

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 01:30:52 ; Search time 124 Seconds
(without alignments)
448.886 Million cell updates/sec

Title: US-10-003-211-1

Perfect score: 1133

Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPEMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1133	100.0	197	2	AAW23220	Aaw23220 Extracell
2	1133	100.0	197	2	AAy31326	Aay31326 Human lym
3	1133	100.0	435	6	ABP96137	Abp96137 Human TNF
4	1133	100.0	435	6	ABR40220	Abrr40220 Human gen
5	1133	100.0	435	6	ABU89821	Abu89821 TNF-recep
6	1129	99.6	399	6	ABP96136	Abp96136 Human TNF
7	1108	97.8	416	7	ADC42856	Adc42856 REMAP pro
8	987	87.1	170	6	ADA49700	Ada49700 Extracell
9	771	68.0	415	4	AAAB36700	Aab36700 Human tum
10	771	68.0	415	6	ABP96138	Abp96138 Mouse lym
11	456	40.2	77	2	AAW94642	Aaw94642 TNF-R ext
12	456	40.2	77	4	AAAB69194	Aab69194 Human TNF
13	381.5	33.7	305	5	ABP41926	Abp41926 Human ova
14	315	27.8	518	2	AAR51003	Aar51003 Sequence
15	311.5	27.5	659	6	ABJ37103	Abj37103 Concatame
16	309	27.3	461	2	AAR72504	Aar72504 p75 Tumou
17	307	27.1	720	6	ABJ37101	Abj37101 Concatame
18	305	26.9	225	3	AAy77463	Aay77463 Primate p
19	305	26.9	225	6	AAO26526	Aao26526 Human tum
20	305	26.9	227	4	AAAB6981	Aab66981 Tnfr2 pro
21	305	26.9	235	2	AAW59665	Aaw59665 Human sol
22	305	26.9	235	2	AAW52270	Aaw52270 Tumour ne
23	305	26.9	235	2	AAW89234	Aaw89234 Tumour ne
24	305	26.9	235	3	AAy54440	Aay54440 Amino aci
25	305	26.9	235	3	AAy54443	Aay54443 Wild type

26	305	26.9	235	4	AAB37685	Aab37685 Human 40
27	305	26.9	235	6	ADA20593	Ada20593 Human 40k
28	305	26.9	248	3	AAy94718	Aay94718 Human typ
29	305	26.9	355	6	ADA09891	Ada09891 Human rec
30	305	26.9	461	2	AAR11141	Aar11141 Human TNF
31	305	26.9	461	2	AAR11001	Aar11001 40KD TNF
32	305	26.9	461	2	AAR42058	Aar42058 Fibroblas
33	305	26.9	461	3	AAB01342	Aab01342 Death rec
34	305	26.9	461	3	AAB18717	Aab18717 A human t
35	305	26.9	461	3	AAB37801	Aab37801 Human tum
36	305	26.9	461	4	AAB35331	Aab35331 Human TNF
37	305	26.9	461	4	AAB37686	Aab37686 Human 40
38	305	26.9	461	4	AAB36698	Aab36698 Human tum
39	305	26.9	461	5	AAU75172	Aau75172 Human TNF
40	305	26.9	461	5	AAU75174	Aau75174 Human TNF
41	305	26.9	461	5	AAU75173	Aau75173 Human TNF
42	305	26.9	461	5	ABP52451	Abp52451 Human tum
43	305	26.9	461	5	ABR55854	Abrr55854 Human tum
44	305	26.9	461	6	ABR39799	Abrr39799 Human DIS
45	305	26.9	461	6	ABO53256	Abo53256 Human tum

ALIGNMENTS

RESULT 1	
AAW23220	
ID	AAW23220 standard; protein; 197 AA.
AC	AAW23220;
XX	
DT	29-OCT-1997 (first entry)
XX	
DE	Extracellular domain of human lymphotoxin beta receptor.
XX	
KW	Human; lymphotoxin beta; receptor; blocking agent; extracellular;
KW	ligand binding; domain; treatment; Thi cell; immune response; delayed;
KW	hypersensitivity; contact; tuberculin; granulomatous; graft versus host;
KW	disease; organ rejection; autoimmune; disorder; multiple sclerosis;
KW	insulin dependent diabetes; uveitis; cytokine; sympathetic ophthalmia;
KW	psoriasis; listeria; Toxoplasma; infection; Mycobacterium; abnormal;
XX	lymphoid organ; development.
OS	
OS	Homo sapiens.
XX	
PN	WO9703687-A1.
XX	
PD	06-FEB-1997.
XX	
PE	19-JUL-1996; 96WO-US012010.
XX	
PR	21-JUL-1995; 95US-00505606.
XX	
PA	(BIOJ) BIOGEN INC.
XX	
PI	Browning JL, Benjamin CD, Hochman PS;
XX	
DR	WPI; 1997-132373/12.
XX	
PT	Compositions comprising lymphotoxin-beta receptor blocking agent - used
PT	to treat auto:immune diseases, e.g. sclerosis, insulin-dependent
PT	diabetes, etc.
XX	
PS	Example 1; Page 55-56; 76pp; English.
XX	
CC	The present sequence, a human lymphotoxin beta receptor (LT-beta-R)
CC	blocking agent, comprises the extracellular ligand binding domain of the
CC	human LT-beta-R up to the transmembrane region. It can be used to treat a
CC	Thi cell mediated immune response which contributes to a delayed type
CC	hypersensitivity reaction, preferably contact, tuberculin type or
CC	granulomatous hypersensitivity, graft versus host disease, organ
CC	rejection or an autoimmune disorder, i.e. multiple sclerosis, insulin
CC	dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can

CC also be used to treat conditions exacerbated by the activities of Th-1
CC type cytokines, or Listeria, Toxoplasma or Mycobacterium infection. Its
CC ability to selectively or partially block the LT-beta-R pathway may be
CC useful in the treatment of abnormal lymphoid organ development associated
CC with misexpression or overexpression of signalling by the LT-beta-R
CC pathway. The present LT-beta-R blocking agent is capable of selectively
CC inhibiting Th1, but not Th2 cell dependent immune effector mechanisms. As
CC Th1 cytokines can inhibit Th2 cell dependent responses, the present LT-
CC beta-R blocking agent may also indirectly stimulate certain Th2 cell
CC dependent responses which are normally inhibited by Th1 induced
CC cytokines. Doses of about 1 mg/kg of the present soluble LT-beta-R are
CC expected to be suitable starting doses for optimising treatment

XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENS 60
Db 1 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENS 60
QY 61 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 120
Db 61 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 120
QY 121 CPPGTEAELEKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
Db 121 CPPGTEAELEKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
QY 181 TTCKNPLEPLPEMSGT 197
Db 181 TTCKNPLEPLPEMSGT 197

RESULT 2
AAV31326
ID AAV31326 standard; peptide; 197 AA.

XX
AC AAV31326;

DT 04-OCT-1999 (first entry)

DE Human lymphotoxin (LT)beta-receptor extracellular region.

KW Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell;
KW immune system; tumour; follicular lymphoma; extracellular domain; human.

OS Homo sapiens.

PN WO938525-A1.

PD 05-AUG-1999.

PF 29-JAN-1999; 99WO-US001928.

PR 30-JAN-1998; 98US-0073112P.

PR 02-FEB-1998; 98US-0073410P.

PA (BIOJ) BIOGEN INC.

PI Browning J, Thorbecke J, Tsiagbe V;

DR WPI; 1999-469242/39.

PT New method of treating follicular lymphomas by inhibiting interaction
PT between lymphotoxin-beta and its receptor.

PS Example 1; Page 25-26; 31pp; English.

XX The invention provides a method for arresting or reducing, severity of
CC effects of a tumour by administration of a composition which inhibits the

CC interaction between lymphotoxin (LT)-beta and its receptor. An inhibitor
CC of the interaction between LT-beta and its receptor can be administered
CC for altering the survival or maintenance of follicular dendritic cells in
CC a subject and for altering the architecture of the organs of the immune
CC system. The method is useful for treating tumours, specifically
CC follicular lymphomas. It offers an alternative therapy for those with
CC tumours resistant to traditional chemotherapy. The present sequence
CC represents the extracellular region of the human LTbeta-receptor and
CC comprises the ligand binding domain

XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENS 60
Db 1 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENS 60
QY 61 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 120
Db 61 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 120
QY 121 CPPGTEAELEKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
Db 121 CPPGTEAELEKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
QY 181 TTCKNPLEPLPEMSGT 197
Db 181 TTCKNPLEPLPEMSGT 197

RESULT 3
ABP96137
ID ABP96137 standard; protein; 435 AA.

XX
AC ABP96137;

DT 09-MAY-2003 (first entry)

DE Human TNF receptor 2 related protein/LTRbeta SEQ ID NO:19.

KW Human, tumour necrosis factor receptor 2 related protein variant;
KW TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;
KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
KW asthma; ulcerative colitis.

OS Homo sapiens.

PN WO2003012037-A2.

PD 13-FEB-2003.

PF 24-JUL-2002; 2002WO-US023684.

PR 27-JUL-2001; 2001US-00917372.

PA (INCY-) INCYTE GENOMICS INC.

PI Lal PG, Warren BA;

DR WPI; 2003-256445/25.

PT New cDNA, useful for preparing a composition for treating a disease or
PT condition associated with increased TNF signalling e.g., cancer of the
PT prostate, ovary, gallbladder, breast, brain, liver or colon, or
PT rheumatoid arthritis, asthma.

PS Disclosure; Fig 2A-C; 64pp; English.

XX The present invention describes human tumour necrosis factor receptor 2
CC related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic

CC and immunosuppressive activities, and can be used in gene therapy. The
CC TNFR2PV CDNA or protein sequences can be used for preparing a composition
CC for treating a disease or condition associated with increased TNF
CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
CC arthritis, asthma or ulcerative colitis. The present sequence represents
CC a human TNFR2 related protein/LTRbeta amino acid sequence, which is given
CC in comparison with human TNFR2PV in the exemplification of the present
CC invention
XX

XX SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPQAVPPYASENQTCRDQEKYEYEPQHRIICSRCPGTYVSAKCSRIRDVTCATCAENS 60
|||
Db 28 SOPQAVPPYASENQTCRDQEKYEYEPQHRIICSRCPGTYVSAKCSRIRDVTCATCAENS 87
QY 61 YNEHWNVYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 120
|||
Db 88 YNEHWNVYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKGNNHCVPCAKGHFQNTSSPSARCQPHTRCENOGLVEAAPGTAQSD 180
|||
Db 148 CPPGTEAELKDEVGKGNNHCVPCAKGHFQNTSSPSARCQPHTRCENOGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPEMSGT 197
|||
Db 208 TTCKNPLEPLPPEMSGT 224

RESULT 4
ABR40220
ID ABR40220 standard; protein; 435 AA.

XX ABR40220;

XX 12-JUN-2003 (first entry)

XX Human genoxin.

KW Human; genoxin; antiarteriosclerotic; antidiabetic; hypotensive;
KW antilipaemic; anorectic; immunomodulator; cytostatic; anti-HIV;
KW antiinflammatory; cardiact; cerebroprotective; gene therapy;
KW tumour necrosis factor receptor; TNFR; body mass; weight loss; obesity.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..30

FT Protein /label= signal_peptide

FT Domain /label= Mature_genoxin

FT Domain /label= Extracellular_domain

FT Domain /label= Transmembrane_domain

FT Domain /label= Intracellular_domain

XX WO2003011322-A1.

XX 13-FEB-2003.

XX 31-JUL-2002; 2002WO-IB003417.

XX 02-AUG-2001; 2001US-0309917P.

XX (GEST) GENSET SA.

XX Lucas J, Dialynas D, Briggs K;

XX WPI; 2003-256417/25.
DR N-PSDB; ABZ99578.

PT Screening for an agonist or antagonist of Genoxin activity, useful for
PT preventing or treating metabolic disorders, comprises contacting Genoxin
PT polypeptide with a test compound and determining binding.

XX Example 10; Page 33-34; 37pp; English.

CC The invention relates to a novel method for screening for an agonist or
CC antagonist of Genoxin activity. The agonists/antagonists of the invention
CC have antiarteriosclerotic, antidiabetic, hypotensive, antilipaemic,
CC anorectic, immunomodulator, cytostatic, anti-HIV, antiinflammatory,
CC cardiact, and cerebroprotective activity. The polypeptides of the
CC invention may have a use in gene therapy, and act as tumour necrosis
CC factor receptor (TNFR) agonists. The method is used to screen for an
CC agonist or antagonist of Genoxin. The method is useful in metabolic
CC research, particularly, in discovering compounds that modulate Genoxin
CC activity or that reduce or increase body mass and maintain weight loss,
CC and in preventing or treating obesity-related diseases or disorders such
CC as hyperlipidaemia, atherosclerosis, heart disease, stroke, insulin-
CC resistant diabetes or hypertension, or for preventing or treating
CC disorders associated with excessive weight loss, such as cachexia, cancer
CC -related weight loss, acquired immunodeficiency syndrome (AIDS)-related
CC weight loss, chronic inflammatory disease-related weight loss, or
CC anorexia. The present sequence represents the human genoxin of the
CC invention
XX

XX SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPQAVPPYASENQTCRDQEKYEYEPQHRIICSRCPGTYVSAKCSRIRDVTCATCAENS 60
|||
Db 28 SOPQAVPPYASENQTCRDQEKYEYEPQHRIICSRCPGTYVSAKCSRIRDVTCATCAENS 87
QY 61 YNEHWNVYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 120
|||
Db 88 YNEHWNVYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKGNNHCVPCAKGHFQNTSSPSARCQPHTRCENOGLVEAAPGTAQSD 180
|||
Db 148 CPPGTEAELKDEVGKGNNHCVPCAKGHFQNTSSPSARCQPHTRCENOGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPEMSGT 197
|||
Db 208 TTCKNPLEPLPPEMSGT 224

RESULT 5
ABU89821
ID ABU89821 standard; protein; 435 AA.

XX ABU89821;

XX 10-JUL-2003 (first entry)

XX TNF-receptor associated factor 5 (TRAF5) interacting protein #1.

XX Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer;

XX TNF-receptor associated factor 5 interacting protein;

XX TRAF5 interacting protein.

XX Homo sapiens.

XX WO2003031571-A2.

XX 17-APR-2003.

PF 02-OCT-2002; 2002WO-US031357.
XX 05-OCT-2001; 2001US-0327454P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 25-JUN-2002; 2002US-0391342P.
PR 01-OCT-2002; 2002US-00262445.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;
PI Edinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R;
PI Mezes PS, Millet I, Ooi CE, Patturajan M, Rieger DK, Spytek KA;
PI Taupier RJ, Zernhusen BD, Zhong H, Zhong M;
XX
DR WPI; 2003-381704/36.
DR N-PSDB; ACA90237.
XX
XX
PT New DAPK3 polypeptide, useful for preparing a composition for treating or
PT preventing e.g., cancer.
XX
PS Example 20F; Page 240; 253pp; English.
XX
CC The invention describes an isolated polypeptide comprising any of 33 90-
CC 1273 amino acid sequences (I) given in the specification or its mature
CC form, a sequence that is at least 95 % identical to (I), or a sequence
CC comprising one or more conservative substitutions in the amino acid
CC sequence of (I). The polypeptide is useful for preparing a composition
CC for treating or preventing e.g. cancer. This is the amino acid sequence
CC of a tumour necrosis factor (TNF)-receptor associated factor 5 (TRAF5)
CC interacting protein associated with the identification of novel human
CC proteins and their functions
XX
SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQPQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENS 60
Db 28 SQPQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENS 87
QY 61 YNEHWNVLTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 120
Db 88 YNEHWNVLTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKGNNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTASD 180
Db 148 CPPGTEAELKDEVGKGNNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTASD 207
QY 181 TTCKNPLEPLPPEMSGT 197
Db 208 TTCKNPLEPLPPEMSGT 224

RESULT 6
ID ABP96136 standard; protein; 399 AA.
XX
AC ABP96136;
XX
DT 09-MAY-2003 (first entry)
XX
DE Human TNF receptor 2 related protein variant SEQ ID NO:1.

XX
KW Human; tumour necrosis factor receptor 2 related protein variant;
KW TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;
KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
KW asthma; ulcerative colitis.
XX
OS Homo sapiens.
XX
PN WO2003012037-A2.
XX
PD 13-FEB-2003.
XX
PF 24-JUL-2002; 2002WO-US023684.
XX
PR 27-JUL-2001; 2001US-00917372.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal PG, Warren BA;
XX
DR WPI; 2003-256445/25.
DR N-PSDB; ABZ79717.
XX
XX
PT New CDNA, useful for preparing a composition for treating a disease or
PT condition associated with increased TNF signaling e.g., cancer of the
PT prostate, ovary, gallbladder, breast, brain, liver or colon, or
PT rheumatoid arthritis, asthma.
XX
PS Claim 20; Fig 1A-F; 64pp; English.
XX
CC The present sequence represents human tumour necrosis factor receptor 2
CC related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic
CC and immunosuppressive activities, and can be used in gene therapy. The
CC TNFR2PV cDNA or protein sequences can be used for preparing a composition
CC for treating a disease or condition associated with increased TNF
CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
CC arthritis, asthma or ulcerative colitis
XX
SQ Sequence 399 AA;

Query Match 99.6%; Score 1129; DB 6; Length 399;
Best Local Similarity 99.5%; Pred. No. 4.3e-78;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQPQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENS 60
Db 28 SQPQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENS 87
QY 61 YNEHWNVLTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 120
Db 88 YNEHWNVLTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKGNNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTASD 180
Db 148 CPPGTEAELKDEVGKGNNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTASD 207
QY 181 TTCKNPLEPLPPEMSGT 197
Db 208 TTCKNPLEPLPPEMSGS 224

RESULT 7
ID ADC42856 standard; protein; 416 AA.
XX
AC ADC42856;
XX
DT 18-DEC-2003 (first entry)
XX
DE REMAP protein #16.
XX
KW Cytostatic; Antiarteriosclerotic; Anti-HIV; Antiinflammatory;

KW Antiallergic; Antidiabetic; REMAP; pathogenesis.
XX
OS Homo sapiens.
XX
PN WO2003027228-A2.
XX
PD 03-APR-2003.
XX
PF 16-JUL-2002; 2002WO-US022833.
XX
PR 17-JUL-2001; 2001US-0306020P.
PR 27-JUL-2001; 2001US-0308179P.
PR 02-AUG-2001; 2001US-0309702P.
PR 10-AUG-2001; 2001US-0311476P.
PR 10-AUG-2001; 2001US-0311551P.
PR 10-AUG-2001; 2001US-0311718P.
PR 24-AUG-2001; 2001US-0314798P.
PR 31-AUG-2001; 2001US-0316639P.
PR 07-SEP-2001; 2001US-0317996P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal PG, Honchell CD, Forsythe IJ, Walia NK, Tang TY, Borowsky ML;
PI Barroso I, Yue H, Warren BA, Thangavelu K, Gietzen KJ, Azimzai Y;
PI lee EA, Baughn MR, Gorvad AE, Duggan BM, Tran B, Li JX;
PI Richardson TW, Elliott VS, Zebartadian Y, Tran UK, Yao MG;
PI Peterson DP, Luo W, Lehr-Mason PM;
XX
DR WPI; 2003-421156/39.
XX
PT New human receptors and membrane-associated proteins (REMAP), useful for
PT diagnosing, treating or preventing disorders associated with aberrant
PT REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or
PT stroke.
XX
PS Claim 1; SEQ ID NO 16; 115pp; English.
XX
CC The present invention relates to an isolated polypeptide. The
CC polypeptides and polynucleotides are useful in diagnosing, treating and
CC preventing disorders associated with aberrant expression of REMAP, such
CC as cell proliferative, autoimmune/inflammatory, renal, neurological,
CC cardiovascular, metabolic, developmental, endocrine, muscle,
CC gastrointestinal, lipid metabolism or transport disorders, and viral
CC infections. These are also useful in assessing the effects of exogenous
CC compounds on the expression of nucleic acids and amino acid sequences of
CC REMAP, in facilitating drug discovery process, and in investigating the
CC pathogenesis of diseases or medical conditions. Expression and
CC purification were achieved using bacterial or virus-based expression
CC systems. The present sequence represents an REMAP protein of the
CC invention.
XX
SQ Sequence 416 AA;

Query Match 97.8%; Score 1108; DB 7; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.8e-76;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 VPPYASENQTRDQEKYEYEPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENSYNEHW 65
Db 14 VPPYASENQTRDQEKYEYEPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENSYNEHW 73
QY 66 NYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRQPGMFCAAMALECTHCELLSDCPGT 125
Db 74 NYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRQPGMFCAAMALECTHCELLSDCPGT 133
QY 126 EAEIKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKN 185
Db 134 EAEIKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKN 193
QY 186 PLEPLPPEMSGT 197
Db 194 PLEPLPPEMSGT 205

RESULT 8
ADA49700
ID ADA49700 standard; protein; 170 AA.
XX
AC ADA49700;
XX
DT 20-NOV-2003 (first entry)
XX
DE Extracellular region of human TNFRRp (htnFRRp) protein.
XX
KW Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity;
KW competitive-type receptor; binding assay; cancer cell; human;
KW TNF receptor family; htnFRRp; cycostatic.
XX
OS Homo sapiens.
XX
PN US2002192729-A1.
XX
PD 19-DEC-2002.
XX
PF 28-MAR-2002; 2002US-00112793.
XX
PR 01-APR-1996; 96US-00625328.
PR 23-SEP-1996; 96US-00710802.
PR 31-MAR-1997; 97US-00828683.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI; 2003-657226/62.
XX
PT Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or
PT Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
PT in diagnostic assays.
XX
PS Disclosure; Fig 2; 53pp; English.
XX
CC The present invention relates to the isolation of a biologically active
CC Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide
CC sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The
CC Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI
CC is useful for generating antibodies, as standards in assays for Apo-3 or
CC Apo-2LI, in affinity purification techniques, and in competitive-type
CC receptor binding assays when labelled with radioiodine, enzymes or
CC fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or
CC inducing apoptosis in cancer cells, and thus have therapeutic utility.
CC The present sequence represents the extracellular region of a human TNF
CC receptor family protein. This sequence is compared with the extracellular
CC region of human Apo-2LI.
XX
SQ Sequence 170 AA;

Query Match 87.1%; Score 987; DB 6; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-67;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TCRDQEKYEYEPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC 74
Db 1 TCRDQEKYEYEPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLC 60
QY 75 RPCDPVMGLEIAPCTSKRKTQCRQPGMFCAAMALECTHCELLSDCPGTEAEIKDEVG 134
Db 61 RPCDPVMGLEIAPCTSKRKTQCRQPGMFCAAMALECTHCELLSDCPGTEAEIKDEVG 120
QY 135 KGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 184
Db 121 KGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 170
RESULT 9
AAB36700

ID	AAB36700 standard; protein; 415 AA.
AC	AAB36700;
XX	
DT	15-MAR-2001 (first entry)
DE	
XX	Human tumour necrosis factor receptor LTBR protein SEQ ID NO:6.
KW	Human, tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic;
KM	TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW	tumour necrosis factor related apoptosis inducing ligand; vasotropic;
KM	immunosuppressive; neuroprotective; antiviral; antinflammatory;
KW	anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KM	gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW	apoptotic cell death related disease; autoimmune disorder;
KM	cardiovascular disorder; viral infection.
XX	
OS	Homo sapiens.
XX	
PN	WO200071150-A1.
XX	
PD	30-NOV-2000.
XX	
PF	18-MAY-2000; 2000WO-US013515.
XX	
PR	20-MAY-1999; 99US-0135164P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Wei Y, Ruben SM, Gentz RL, Ni J;
XX	
DR	WPI; 2001-041051/05.
XX	
PT	Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT	necrosis factor receptor 5, useful in the diagnosis, treatment or
PT	prevention of cancer, autoimmune disorders and viral infection.
XX	
PS	Disclosure; Fig 2; 285pp; English.
XX	
CC	The present invention describes the human TRID protein (tumour necrosis
CC	factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC	intracellular domain, also referred to as tumour necrosis factor receptor
CC	5 (TNFR-5 or TR5)). TRID has cytosstatic, immunosuppressive, nootropic,
CC	neuroprotective, antiviral, antinflammatory, anticonvulsant,
CC	antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC	activities, and can be used in gene therapy. The TRID polynucleotides are
CC	useful for detecting complementary polynucleotides. TRID proteins and
CC	polynucleotides are useful in the treatment of tumours, resistance to
CC	parasite, bacteria and viruses, restenosis and graft versus host disease.
CC	They are also useful for inducing proliferation of T-cells, endothelial
CC	cells and certain haematopoietic cells, to regulate antiviral responses
CC	and to prevent certain autoimmune diseases after stimulation of TRID by
CC	an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC	polypeptides are useful for treating and/or preventing diseases
CC	associated with increased or decreased apoptotic cell death. The TRID
CC	polynucleotides, proteins, antibodies, agonists and antagonists are
CC	useful in the diagnosis, treatment or prevention of: (a) cancer; (b)
CC	autoimmune disorders; (c) diseases associated with increased apoptosis;
CC	(d) cardiovascular disorders; and (e) viral infection. The present
CC	sequence represents a tumour necrosis factor receptor used in comparison
CC	with TRID in the exemplification of the present invention
XX	
SQ	Sequence 415 AA;
<hr/>	
Query Match	68.0%; Score 771; DB 4; Length 415;
Best Local Similarity	70.7%; Pred. No. 8.4e-51;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1	
QY	1 SGPQAVPPYASENQTCRDQEKEYEPOHRICSRCPGTYVSAAKCSRIRDTVCATCAENS 60 : : : : Db 28 SQPLVPFPRIENQTCWDQDKXEYEPMDVCCSRCPPGEFFFAVCSRSQDTVCKTCEPHNS 87
QY	61 YNEHMNYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAAMALECTHC--ELL 118

[illegible]

Db 88 YNEHWNHLSTCQLCRPCDIVLGFEVAPCTSDRKAECRCQPGMGCYYLDNECVHCEEBRL 147
QY 119 SDCCPPTGEAEIKDEVGKGNHCVPCXAGHFQNTSSPSARCCQPHTRCENQGLVEAAPGTAQ 178
Db 148 VLCQPGTEAEVTDIMDTDVNCVPCRGHFQNTSSPRARCQPHTRCEIQGLVEAAPGTSY 207
QY 179 SDTCKNPLEP 189
Db 208 SDTCKNPPPEP 218

RESULT 11

AAW94642
ID AAW94642 standard; peptide; 77 AA.
XX
AC AAW94642;
XX
DT 29-APR-1999 (first entry)
XX
DE TNF-R extracellular Cys-rich domain TNF-R-rp.
XX
KW Tumour necrosis factor receptor; TNF-R; autoimmune diseases;
KW inflammation; septic shock; cachexia; graft versus host disease;
KW skin allergic reaction; immune complex disease; malaria;
KW transplantation rejection.
XX
OS Homo sapiens.
XX
PN WO9853842-A1.
XX
PD 03-DEC-1998.
XX
PF 29-MAY-1998; 98WO-US010891.
XX
PR 30-MAY-1997; 97US-00866545.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Greene MI, Murali R, Takasaki W;
XX
DR WPI; 1999-080781/07.
XX
PT New compounds designed from a binding loop of a tumour necrosis factor
PT receptor - are capable of inhibiting the biological activities of tumour
PT necrosis factor, e.g., in treating inflammation or autoimmune diseases.
XX
PS Disclosure; Fig 1; 78pp; English.
XX
CC The present invention describes peptides and peptide analogues which
CC correspond in primary sequence to a binding loop of a tumour necrosis
CC factor receptor (TNF-R) superfamily member. The compounds are especially
CC designed from a binding loop of TNF-R p55. They are capable of inhibiting
CC TNF binding to its cellular receptors and may be used to inhibit the
CC biological activities of TNF. They may be used in treating TNF-associated
CC conditions such as acute and chronic inflammatory responses, septic
CC shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic
CC reactions, immune complex disease, transplantation rejection and malaria.
CC Administration is, e.g. oral, transdermal, transmucosal, pulmonary,
CC subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5
CC mg/kg/day. The present sequence represents an extracellular Cys-rich
CC domain of TNF-R from the present invention
XX
SQ Sequence 77 AA;

Query Match 40.2%; Score 456; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNHWNLYLTICQLCRPCDPVMGLEEIAICTSKRKTQCRQCPGMFCAAWALE 111
Db 1 VCATCAENSYNHWNLYLTICQLCRPCDPVMGLEEIAICTSKRKTQCRQCPGMFCAAWALE 60

QY 112 CTHCELLSDCPPTGEAE 128
Db 61 CTHCELLSDCPPTGEAE 77

RESULT 12

AAB69194
ID AAB69194 standard; protein; 77 AA.
XX
AC AAB69194;
XX
DT 30-APR-2001 (first entry)
XX
DE Human TNF-R extracellular Cys-rich domain TNF-R-rp SEQ ID NO:3.
XX
KW Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
KW osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic;
KW antirheumatic; antiarthritic; antiinflammatory; immunomodulatory;
KW tumour necrosis factor-related activation-induced cytokine; TRANCE;
KW receptor activator of NF-kappaB ligand; RANK; osteoporosis;
KW Paget's disease; metastatic bone disease; rheumatoid arthritis;
KW periodontal disease; modulating dendritic cell maturation;
KW T cell proliferation; CD40 receptor system.
XX
OS Homo sapiens.
XX
PN WO200108699-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-US020510.
XX
PR 28-JUL-1999; 99US-0146090P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
PA (AOKI/) AOKI K.
PA (HORN/) HORNE W C.
PA (BARO/) BARON R.
XX
PI Aoki K, Horne WC, Baron R, Greene MI, Murali R;
XX
DR WPI; 2001-182866/18.
XX
PT Use of peptides and peptide analogs which are TRANCE/RANK inhibitors, for
PT inhibiting osteoclastogenesis and bone resorption.
XX
PS Disclosure; Fig 1; 81pp; English.
XX
CC The present invention describes a method for inhibiting
CC osteoclastogenesis and bone resorption. Osteoclastogenesis and bone
CC resorption inhibiting peptide analogues from the present invention have
CC osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory
CC and immunomodulatory activities, and are tumour necrosis factor (TNF)-
CC related activation-induced cytokine (TRANCE)/ receptor activator of NF-
CC kappaB ligand (RANK) inhibitors. The method is useful for treating
CC diseases characterised by bone loss such as osteoporosis, Paget's
CC disease, metastatic bone disease, rheumatoid arthritis or periodontal
CC disease, and modulating dendritic cell maturation, T cell proliferation,
CC and/or CD40 receptor systems. The present sequence represents an
CC extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-
CC R) superfamily member, which is used in the exemplification of the
CC present invention
XX
SQ Sequence 77 AA;

Query Match 40.2%; Score 456; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNHWNLYLTICQLCRPCDPVMGLEEIAICTSKRKTQCRQCPGMFCAAWALE 111
Db 1 VCATCAENSYNHWNLYLTICQLCRPCDPVMGLEEIAICTSKRKTQCRQCPGMFCAAWALE 60

0Y 112 CTHCELLSDCPGTEAE 128
 |||||
 Db 61 CTHCELLSDCPGTEAE 77
 RESULT 13
 ID ABP41926 standard; protein; 305 AA.
 AC ABP41926;
 DT 22-AUG-2002 (first entry)
 DE Human ovarian antigen HSABJ44, SEQ ID NO:3058.
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 12p13.
 OS Homo sapiens.
 PN WO200200677-A1.
 PD 03-JAN-2002.
 PF 07-JUN-2001; 2001WO-US018569.
 PR 07-JUN-2000; 2000US-0209467P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Birse CE, Rosen CA;
 DR WPI; 2002-147878/19.
 DR N-PSDB; ABQ55003.
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 XX Claim 11; SEQ ID NO 3058; 2922pp; English.
 XX
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovarian and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the

```
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 305 AA;

Query Match          33.7%; Score 381.5; DB 5; Length 305;
Best Local Similarity 93.4%; Pred. No. 2.9e-21;
Matches 71; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY      123 PGTEA-ELKDEVGKNNHCVPCKAGHPONTSSPSARCOPHTRCENOGLV EAAPGTASDT 181
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       19 PGWPAFLPDEVGKNNHCVPCKAGHFONTSSPSARCOPHTRCENOGLV EAAFGTASDT 78

QY      182 TCKNPLEPLPPEMSGT 197
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       79 TCKNPLEPLPPEMSGT 94

RESULT 14
AAR51003
ID AAR51003 standard; protein, 518 AA.
XX
AC AAR51003;
XX
DT 25-MAR-2003 (revised)
DT 07-OCT-1994 (first entry)
XX
DE Sequence of a recombinant human (rhu) tumour necrosis factor receptor
DE TNFR/fc fusion protein.
XX
KM Tumour necrosis factor receptor; chimeric antibody molecule;
KW immunoglobulin.
XX
OS Synthetic.
XX
PN WO9406476-A1.
XX
PD 31-MAR-1994.
XX
PF 14-SEP-1993; 93WO-US008666.
XX
PR 15-SEP-1992; 92US-00946236.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Smith CA, Jacobs CA;
DR WPI, 1994-118172/14.
XX
DR N-PSDB; AAQ45225.
PT Treating TNF mediated inflammatory diseases with TNF antagonist - esp.
PT soluble form of TNF receptor, opt. as fusion protein with human
PT immunoglobulin Fc region, esp. for treating arthritis.
XX
PS Disclosure; Page 32-34; 47pp; English.
XX
AAQ45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast
CC cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein
CC having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for TNFRI
CC was described in Smith et al., Science 248:1019,1990. Clone 1 is
CC contained in expression vector pCAV/NOT-TNFR (ATCC 68088). A recombinant
CC chimeric antibody may be produced having TNFR sequences substituted for
CC the variable domains of either or both of the immunoglobulin molecule
CC heavy and light chains and having unmodified constant region domains. A
CC specific example of a TNFR/Fc fusion protein is given in AAQ45225/R51003.
CC The rhu TNFR:Fc fusion gene was created by ligating the following
CC fragments into a cloning vector: 1) an 867 bp Asp718-Pvu2 fragment from
CC pCAV/NOT-TNFR (ATCC 68088) contg. the cDNA encoding the truncated TNFR.
CC 2) a 700 bp StyI-SpeI fragment from plasmid PIXY498 coding for 232 AAs of
```


CC the Fc portion of human IgG1. Plasmid pIXY498 is a yeast expression
CC vector contg. the Fc fragment of human IgG1. 3) An oligo linker, to fuse
CC the truncated TNFR with the human IgG1 Fc fragment. This linker was
CC created by PCR using primer AAQ45226, which encodes the 3' end of the
CC truncated TNF receptor and the 5' end of human IgG1, and primer AAQ45227,
CC which is an antisense sequence encoding bps 257-237 of human IgG1.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ

Sequence 518 AA;

Query Match 27.8%; Score 315; DB 2; Length 518;
Best Local Similarity 35.5%; Pred. No. 5.9e-16;
Matches 71; Conservative 24; Mismatches 77; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTCRDQEKYEYEPQHRICCSRCPPGTYYSAKCSRIKDTVCATCAENSYNE 63
Db 57 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKEVCTKTSDDTVCDSCEDSTYTQ 114
QY 64 HNNYLITICQLCR--PCDPVWGLEIEIAPCTSKRKTKQCRCPGMFCAAWALE-CTHCELLS 119
Db 115 LNMWVPECLSCGSRCSDDV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 170
QY 120 DCPFG-----TEAEIKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
Db 171 KCRPGFGVAPRGTEITSDV-----CKPCAPGTFSTNTSTIDICRPHQICN---VVAIP 220
QY 175 GTAQSDTTC--KNPLEPLRP 192
Db 221 GNASMDAVCTSTSPTRSMAP 240

RESULT 15

ABJ37103
ID ABJ37103 standard; protein; 659 AA.

AC ABJ37103;

DT 08-MAY-2003 (first entry)

DE Concatameric immunoadhesion human protein sequence SEQ ID No 12.

XX Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human.

OS Homo sapiens.

XX WO2003010202-A1.

XX 06-FEB-2003.

XX 26-JUL-2002; 2002WO-KR001427.

XX 26-JUL-2001; 2001KR-00045028.

XX (MEDE-) MEDEXGEN CO LTD.

XX Chung Y, Han J, Lee H, Choi E, Kim J;

XX WPI; 2003-229639/22.

XX N-PSDB; ABT32046.

XX New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.

PS Claim 27; Page 148-152; 21pp; English.

XX The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical

CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC related diseases. This sequence represents the human concatameric protein
CC of the invention
XX
SQ

Sequence 659 AA;

Query Match 27.5%; Score 311.5; DB 6; Length 659;
Best Local Similarity 36.4%; Pred. No. 1.4e-15;
Matches 71; Conservative 23; Mismatches 74; Indels 27; Gaps 9;

QY 5 AVPPYASE-NQTCRDQEKYEYEPQHRICCSRCPPGTYYSAKCSRIKDTVCATCAENSYNE 63
Db 28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKEVCTKTSDDTVCDSCEDSTYTQ 85
QY 64 HNNYLITICQLCR--PCDPVWGLEIEIAPCTSKRKTKQCRCPGMFCAAWALE-CTHCELLS 119
Db 86 LNMWVPECLSCGSRCSDDV----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 141
QY 120 DCPFG-----TEAEIKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
Db 142 KCRPGFGVAPRGTEITSDV-----CKPCAPGTFSTNTSTIDICRPHQICN---VVAIP 191
QY 175 GTAQSDTTCKNPLEP 189
Db 192 GNASMDANCTSP-EP 205

Search completed: August 28, 2004, 01:47:03
Job time : 129 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 01:43:28 ; Search time 40 Seconds
(without alignments)
473.743 Million cell updates/sec

Title: US-10-003-211-1
Perfect score: 1133
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTCKNPLEPLPEMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	435	2 I54182	tumor necrosis fac
2	305	26.9	461	1 A35356	tumor necrosis fac
3	295	26.0	474	2 B38634	tumor necrosis fac
4	290	25.6	459	2 I48854	gene murine tumour
5	278	24.5	277	2 A60771	B-cell activation
6	243.5	21.5	305	2 A46476	B cell-associated
7	226.5	20.0	651	2 JC7705	death receptor-6 -
8	222.5	19.6	271	2 S12783	OX40 antigen precu
9	214.5	18.9	272	2 I48700	gene ox40 protein
10	210.5	18.6	455	1 GQHUT1	tumor necrosis fac
11	210	18.5	348	2 T28623	hypothetical prote
12	210	18.5	349	2 D36858	gene G4R protein -
13	207	18.3	349	2 D72175	G2R protein - vari
14	206	18.2	461	2 JC4302	tumor necrosis fac
15	201	17.7	277	2 I37552	OX40 homolog - hum
16	201	17.7	454	1 GQMS1	tumor necrosis fac
17	196	17.3	595	2 A42086	CD30 antigen precu
18	195.5	17.3	255	2 I38426	lymphocyte activat
19	189	16.7	325	2 B43692	T2 protein - rabbi
20	187.5	16.5	314	2 I37383	FAS soluble protei
21	184.5	16.3	461	1 GQRTT1	tumor necrosis fac
22	183.5	16.2	326	1 GQVZML	T2 protein - myxom
23	181	16.0	335	2 A40036	apoptosis-mediati
24	179.5	15.8	256	2 B32393	T-cell antigen 4-1
25	171.5	15.1	425	1 A26431	nerve growth facto
26	166	14.7	493	2 JC5486	membrane glycoprot
27	164	14.5	416	1 JN0006	nerve growth facto
28	162	14.3	327	2 A46484	apoptosis-mediati
29	148.5	13.1	427	1 GQHUN	nerve growth facto

30	145.5	12.8	324	2 JC2395	Fas antigen precu
31	133	11.7	260	1 A46517	CD27 antigen precu
32	132.5	11.7	1111	2 T26972	hypothetical prote
33	129.5	11.4	1620	2 T27283	hypothetical prote
34	129	11.4	3084	1 MMSA	laminin alpha-1 ch
35	128.5	11.3	1299	2 T43251	furin (EC 3.4.21.7
36	128	11.3	1274	2 T42017	cysteine rich prot
37	126	11.1	3635	2 T10053	laminin alpha 5 ch
38	125.5	11.1	2180	2 T29764	hypothetical prote
39	124.5	11.0	899	2 G02428	subtilisin-like pr
40	124.5	11.0	915	2 JC6148	subtilisin-like pr
41	124.5	11.0	3707	2 S18252	heparan sulfate pr
42	124	10.9	1680	2 A43434	furin (EC 3.4.21.7
43	123.5	10.9	686	2 JC7569	Delta-4 protein -
44	123	10.9	722	2 I48324	DELTA-like 1 - mou
45	122.5	10.8	915	1 A48225	subtilisin-like pr

ALIGNMENTS

RESULT 1
I54182
tumor necrosis factor receptor 2-related protein - human
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C/Accession: I54182
R/Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A/Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequ
A/Reference number: I54182; MUID:93252381; PMID:8486360
A/Accession: I54182
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-435 <RES>
A/Cross-references: GB:I04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C/Genetics:
A/Gene: GDB:LTBR
A/Cross-references: GDB:1230195; OMIM:600979
A/Map position: 12p13.3-12p13.1
C/Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 100.0%; Score 1133; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SQPQAVPPYASENQTCRDQEKEYEYEPQHRICSCRCPGTYVSACSRIRDTVCATCAENS 60		121	CPPGTEAEIKDEVGKGNHCVPCXAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB	28	SQPQAVPPYASENQTCRDQEKEYEYEPQHRICSCRCPGTYVSACSRIRDTVCATCAENS 87		148	CPPGTEAEIKDEVGKGNHCVPCXAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY	61	YNEHWNVLTICQLCRPCDPVMGLEETAPCTSKRKTQCRCQPGMFCAMALBCTHCELLSD 120		181	TTCKNPLEPLPEMSGT 197
DB	88	YNEHWNVLTICQLCRPCDPVMGLEETAPCTSKRKTQCRCQPGMFCAMALBCTHCELLSD 147		208	TTCKNPLEPLPEMSGT 224

RESULT 2
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N/Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 27-Oct-2003
C/Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R/Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S
Science 248, 1019-1023, 1990
A/Title: A receptor for tumor necrosis factor defines an unusual family of cellular ar

A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring
A;Reference number: A36475; MUID:91045991; PMID:2172983
A;Accession: A36475
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-195,'R',197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A;Reference number: A48416; MUID:91370690; PMID:1966549
A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 23-461 <DEM>
A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:P:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A;Reference number: A36007; MUID:90349572; PMID:2166946
A;Accession: A36007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A;Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A;Reference number: A23666; MUID:91056048; PMID:2173696
A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40;65-69;136-141;300-306 <LOE>
R;Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934; PMID:7821811
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C;Genetics:
A;Gene: GDB:TNFR2
A;Cross-references: GDB:I25914; OMIM:191191
A;Map position: 1p36.2-1p36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>

```
F;262-279/Domain: #status predicted <TMN>
F;280-461/Domain: #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) #status predicted
```

Query Match	26.9%	Score 305;	DB 1;	Length 461;
Best Local Similarity	35.0%	Pred. No. 6.1e-16;		
Matches 70;	Conservative 24;	Mismatches 78;	Indels 28;	Gaps 9;

QY 5 AVPEYASE-NQTCRDQEEKEYEBOHRICCSRCPPGTYVSAKCSRIRDYVCATCAENSINE 63
| | | | : | | : | | : | | : | | : | | :
Db 28 AFTPYAPEPGSTCR--LREYIDQTAQMCCSKCSPGQHAKEVCTKTSIDTVCDSCDCESTYTQ 85

```

QY      64  HMYLTICQLCR---PCDDPMGLEETAPCTSKRKTQCRCQOPGMFCAMALE-CTHCELLS  119
      ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     86  LMMWPECLSCGRSSDQV---ETQACTREQNRICTRPGWYCALSKQEGCRUCAPLR  141

```

QY 120 DCPFG-----TEAEIKDEVGKGNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAP 174
| | | | | : : : |
Db 142 KCRPFGVGVARPGTETSDV-----CKPCAPGTFSNTTTSSTDCIRPHQICN----VVAIP 191

```

QY      175 GTAQSDTTC--KNPLEPLPP 192
          ||| | :| :|
Db      192 GNASMDAVCTSTSPTRSMAP 211

```

RESULT 3

tumor necrosis factor receptor type 2 precursor - mouse

```
C:\species: Mus musculus (mammal m000001)
C:\Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 27-Oct-2003
```

R; Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E

A; Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor

A;Accession: B38634

A:Residues: 1-474 <LEW>

MoJ. Cell. Biol. 11, 3020-3026, 1991

A:Reference number: AA0254; MUID:91246168; PMID:1645445

A; accession: AF0233
A; molecule type: mRNA

A; residues: 1-174 ~ 1000
A; Cross-references: GB:M60469; NID:q199827; PIDN:AAA39752.1; PID:q199828

submitted to the EMBL Data Library, May 1995

A;Reference number: S54816

A; Status: preliminary

A;Residues: 1-22 <KIS>

C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homo-

```
F;1-22/Domain: signal sequence #status predicted <SIG>
```

F;40-77/Domain: NGF receptor repeat homology <NG1>

F,166-203/Domain: NGF receptor repeat homology <NG4>

Query Match	26.0%;	Score 295;	DB 2;	Length 474;
Best Local Similarity	34.0%;	Pred. No. 3.5e-15;		
Matches 66;	Conservative 24;	Mismatches 84;	Indels 20;	Gaps 8;

8 PYASE-NQTCRDEKEYEPQHRICCSRCPPTVVSAKCSRIRDVCAICAENSYNENHN 66

Db 31 PYKPEPGYCQISQ-EYYDRKAQMCACKCPGQYVKHFCNKTSDTVCAACEASMYTQVWN 89

67 YLTICQLCR---PCDPVMGLEIAPCTSKRKTQCRCQPGMCA--AMALECTHCELLSDC 121

Db 90 QFRTCLSCSSSCTDQV---EIRACTKQQNRYVACAEAGRYCALKTHSGSCRCQMLSKC 145
QY 122 PPGTEAEIKDEVGKGNHNCVPCAKGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDT 181
Db 146 GPGF-GVAASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRICS---ILAIFGNASTDA 200
QY 182 TCKNPLEPLPEMS 195
Db 201 VC---APESPTLS 210

RESULT 4
148854

Gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 27-Oct-2003
C/Accession: I48854
R.Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A/Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A/Reference number: I48854; MUID:95178848; PMID:7873884
A/Accession: I48854
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-459 <RES>
A/Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C/Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 25.6%; Score 290; DB 2; Length 459;
Best Local Similarity 33.5%; Pred. No. 8.2e-15;
Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;

QY 8 PYASE-NQTCRDQEKYEYPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNHWN 66
Db 16 PYKPEEGYECQISQ-EYYDRKQMCCKACPKPGQYVKHFCNKTSIDTVCADCEASMTQVMN 74
QY 67 YLTTCQLCR--PCDPVMGLEELAPCTSKRKTQCRCQPGMFGA--AWALECTHCELLSDC 121
Db 75 QFRTCLSCSSSCTDQV---EIRACTKQQNRYVACAEAGRYCALKTHSGSCRCQMLSKC 130
QY 122 PPGTEAEIKDEVGKGNHNCVPCAKGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDT 181
Db 131 GPGF-GVAASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRICS---ILAIFGNASTDA 185
QY 182 TCKNPLEPLPEMS 195
Db 186 VC---APESPTLS 195

RESULT 5

A60771
B-cell activation protein CD40 precursor - human
N/Alternate names: B-cell surface antigen Bp50
C/Species: Homo sapiens (man)
C/Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C/Accession: S04460; A60771
R.Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A/Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A/Reference number: S04460; MUID:89356608; PMID:2475341
A/Accession: S04460
A/Molecule type: mRNA
A/Residues: 1-277 <STA>
A/Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R.Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A/Title: Biochemical characteristics and partial amino acid sequence of the receptor-link
A/Reference number: A60771; MUID:89093941; PMID:2463309
A/Accession: A60771
A/Molecule type: protein
A/Residues: 21-50 <BRA>

A/Experimental source: Burkitt lymphoma cell line Raji
C/Genetics:

A/Gene: GDB:CD40
A/Cross-references: GDB:215268; OMIM:109535
A/Map position: 20q12-20q13.2
C/Superfamily: CD27 antigen; NGF receptor repeat homology
C/Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prote
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TMM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.5%; Score 278; DB 2; Length 277;
Best Local Similarity 35.0%; Pred. No. 4.4e-14;
Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

QY 7 PPYASENQTCRDQEKYEYPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNHWN 66
Db 22 PPTA-----CR--EKQYLINSQ--CCSLCQPGQKLVSDCTEFTEPTECLPCGESEFLDTWN 72
QY 67 YLTTCQLCRPCDPVMGLEELAPCTSKRKTQCRCQPGMFGAAMALECTHCELLSDCPGTE 126
Db 73 RETHGHQHKYCDPNLGLRVQQKGTSETDTICTCEGWHCTSEA--CESVLHRSCSPGFG 130
QY 127 AEIKDEVGKGNHNCVPCAKGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 183
Db 131 VK-QIATGVSDTICEPCPVGFPSNVSSAFKCHPWTSCETKDILVVQAGTKNTDVC 186

RESULT 6

A46476
B cell-associated surface molecule CD40, long splice form - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C/Accession: A46476; A46515
R.Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A/Title: Differential increase of an alternatively polyadenylated mRNA species of mur
A/Reference number: A46476; MUID:92105763; PMID:1370315
A/Accession: A46476
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-305 <TOR>
A/Cross-references: GB:M83312; NID:g1553058
A/Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:75207)
A/Note: this translation is not annotated in GenBank entry, MUSCD40A, release 113.0
R.Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayn
J. Immunol. 149, 3921-3926, 1992
A/Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A/Reference number: A46515; MUID:93094586; PMID:1281194
A/Accession: A46515
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-287, 'LV' <GRI>
A/Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126;
A/Experimental source: BALB/c, liver
A/Note: sequence extracted from NCBI backbone (NCBIP:120357)
C/Comment: For an alternative splice form, see PIR:A46515.
C/Comment: For an alternative splice form, see PIR:A46476.
C/Superfamily: CD27 antigen; NGF receptor repeat homology
C/Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 21.5%; Score 243.5; DB 2; Length 305;
Best Local Similarity 31.0%; Pred. No. 1.9e-11;
Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;

QY 15 TCRDQEKYEYPQHRICSRCPGTYVSACSRIRDTVCATCAENSYNHWNYLITCQLC 74
Db 25 TCSD--KQYLHDGQ--CCDLQCPGSRILTSHTALEKTQCHPCDSGSEFSQAWNREIRCHQH 80

```

QY      75 RCPDPMGLEIETAPCTSKRKTQCRCQPGMFCAAMALECTHCELLSDCPPG-----TEAEI 129
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      81 RHCEPNÖGLRVKKEGTAEISDTVCTCKEGQHCT--SKDCCEACAGHTPCIPFGVMEMATET 138

QY      130 KDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENÖGLVEAAPGTAQSDTTC 183
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      139 TDTV-----CHPCPVGVGFSSNQSLEFKCYPWTSCEDKNLEVLÖKGTSTQTNVIC 186

RESULT 7
JC7705
death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003
C;Accession: JC7705
R;Bridgeham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705; MUID:21308433; PMID:11414698
A;Accession: JC7705
A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
to the TNFR superfamily, which activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: ovary
F;1-21/Domains: signal sequence #status predicted <SIG>
F;52-196/Domains: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domains: transmembrane #status predicted <TM>
F;410-475/Domains: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

Query Match          20.0%; Score 226.5; DB 2; Length 651;
Best Local Similarity 28.8%; Pred. No. 6.5e-10;
Matches 49; Conservative 26; Mismatches 62; Indels 33; Gaps 6;

QY      30 ICCSRCPPTGYVSAACSRIRDTVCATCAENSYNHEHWNYLTICQLCR-PDPMGLEIETAP 88
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      50 LICDKCPAGTYVSKHCTKSLRECSPPBDGTFTHKHENGIERCHRCRPCE--LPMIEKTH 107

QY      89 CTSKRKTQCRCQPMF-----CAAMALECTHCELLSDCP-----PGTEALKDEVGKG 136
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      108 CTALTIRECTCTLSGTFOINDTCVPTYV-----CPVGMGVRRKKGTETE----- 149

QY      137 NNHCVPCKAGHFQNTSSPSARCQPHTRCENÖGLVEAAPGTAQSDITCKNP 186
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      150 DVRCKPCLRGFTFSVPSSVMCKXTYDCFGKNMVVVKPGTKESDNVCKXP 199

RESULT 8
OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
A;Reference number: S12783; MUID:90214614; PMID:2157591
A;Accession: S12783
A;Molecule type: mRNA
A;Residues: 1-271 <MAL>
A;Cross-references: EMBL:X17037; NID:g57830; PIDD:CAA34897.1; PID:g57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domains: signal sequence #status predicted <SIG>
F;20-271/Product: OX40 antigen #status predicted <MAT>
F;211-235/Domains: transmembrane #status predicted <TM>

```

	Query Match	19.6%; Score 222.5; DB 2; Length 271;
	Best Local Similarity	32.1% ; Pred. No. 6.7e-10; Mismatches 68; Indels 27; Gaps 5;
	Matches	53; Conservative 17; Mismatched 68; Indels 27; Gaps 5;
OY	21 KEYEPEQHRICCSRCPPTGTVSAAKSRIRDTVCATCAENSYNHEWNYLTTCQLCRPCDPV	80
	: : : : : : :	:
Dn	28 KDTYPSSGHK-CCECOPGHGMVSRCDHTRDVTCHPCEPGFYNEAVNVDT-CKOCTOCNHR	85
OY	81 MGLEETAPCTSRRKTQCRCQPQMFCAMALECTHCELLSDCPPGTAEALKDEVKGNNHC	140
	: : : : : :	:
Dn	86 SGSELKNONCTPTEDIVCQR-----PQTQPR-QDSHGKLGVDC	122
OY	141 VPCKAGHFONTSSPSARCQHPTRCENOGIVEAAPTQAOSDTICKN	185
	:~::~: :: :	: :
Dn	123 VPCPPGFHSFGSNQA--CKPWNTCTLGGKJRHDAASNSLDTVCED	165
RESULT 9		
	gene OX40 protein - mouse	
	N;Alternate names: OX40 antigen	
C;Species:	Mus musculus (house mouse)	
C:date:	02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 11-Jan-2000	
C;Accession:	I48700; I48334; S34377	
R;Calderhead,	D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.	
J;Immunol.	151, 5261-5271, 1993	
A>Title:	Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int	
A;Reference number:	I48700; MIDID:94044750; PMID:8228223	
A;Accession:	I48700	
A>Status:	translated from GB/EMBL/DDBJ	
A:Molecule type:	mRNA	
A;Residues:	1-272 <RES>	
A;Cross-references:	EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828	
B;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.		
Eur. J. Immunol.	25, 926-930, 1995	
A>Title:	Gene structure and chromosomal localization of the mouse homologue of rat OX40	
A;Reference number:	I48334; MIDID:95255413; PMID:7737295	
A;Accession:	I48334	
A>Status:	translated from GB/EMBL/DDBJ	
A:Molecule type:	DNA	
A;Residues:	1-14,'G','16-272 <RE2>	
A;Cross-references:	EMBL:X85214; NID:g732818; PIDN:CAB59476.1; PID:g732819	
C;Genetics:		
A;Gene:	ox40	
A;Intons:	45/1; 86/1; 122/1; 144/2; 210/1; 250/1	
C;Superfamily:	CD27 antigen; NGF receptor repeat homology	
Query Match	18.9%; Score 214.5; DB 2; Length 272;	
Best Local Similarity	31.7%; Pred. No. 2.7e-09;	
Matches	53; Conservative 16; Mismatches 67; Indels 31; Gaps 6;	
OY	21 KEYEPEQHRICCSRCPPTGTVSAKSRIRDTVCATCAENSYNHEWNYLTTCQLCRPCDPV	80
	: : : : : :	:
Dn	29 KHTPSPSGHK-CRECOPGHGMVSRCDHTRDVLCHPCETGYNEAVNVDT-CKOCTOCNHR	86
OY	81 MGLEETAPCTSRRKTQCRCQPQMFCAMALECTHCELLSDCPPGTAEALKDEVKGNNHC	140
	: : : : : :	:
Dn	87 SGSELKONCTPTQDVCR-----PQTQPR-QDSGYTLGVDC	123
OY	141 VPCKAGHFONTSSP-SARCOPTHRCENOGLVEAAPGTAQSDDTTCKN	185
	:~::~: :: :	: :
Dn	124 VPCPPGFH----SPENNQA CKPWTNCTLSGKOTRHPASDSLDAVGED	166
RESULT 10		
GQUHTI	tumor necrosis factor receptor 1 precursor [validated] - human	
N;Alternate names:	P55 tumor necrosis factor receptor; TNF receptor type 1	
N;Contains:	tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prote	
C;Species:	Homo sapiens (man)	
C:date:	30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 08-Dec-2000	
C;Accession:	A38208; A34899; A34900; A36555; C36555; A38281; SL2057; DT0758; A60231; A	
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.		

```

Query Match      19.6%; Score 222.5; DB 2; Length 271;
Best local similarity 32.1%; Pred. No. 6.7e-10;
Matches 53; Conservative 17; Mismatches 68; Indels 27; Gaps 5;

OY      21 KEYYPEPQHRICCSRCPGTYVSAKCSRIRDVTCATCAENSYNHEWNYLTICQLCRPCDPV 80
      28 KDTYPSGSK-CCRECQPGHGMVSRCDHTRDVTCHPCBPGFYNEAVNYDT-CKQCTQCNRH 85
      81 MGLEETAPCTSKRKTQCRQCPGMFCAMALBCTHCELLSDCPGTEAEIKDEVGKGNHC 140
      86 SGSELKQNCPTPTEDTVCCQCR-----PGTQPR-QDSHKLGVDC 122
      DB      141 VPCKAGHPQNTSSPSARCPQPHTRCENQGLVEAAPGTAQSDTTCKN 185
      123 VPCPPGHFSPGSNQ--CKPWTNCTLSGKQIRHPASNSLDTVCED 165

RESULT 9
148700
gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; J54377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell int
A;Reference number: I48700; MUID:94044750; PMID:8228223
A;Accession: I48700
A;Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A;Reference number: I48334; MUID:95255413; PMID:7737295
A;Accession: I48334
A;Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-14, 'G', 16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match      18.9%; Score 214.5; DB 2; Length 272;
Best local similarity 31.7%; Pred. No. 2.7e-09;
Matches 53; Conservative 16; Mismatches 67; Indels 31; Gaps 6;

OY      21 KEYYPEPQHRICCSRCPGTYVSAKCSRIRDVTCATCAENSYNHEWNYLTICQLCRPCDPV 80
      29 KHTYPSGSK-CCRECQPGHGMVSRCDHTRDVTLCPCETGFYNEAVNYDT-CKQCTQCNRH 86
      81 MGLEETAPCTSKRKTQCRQCPGMFCAMALBCTHCELLSDCPGTEAEIKDEVGKGNHC 140
      87 SGSELKQNCPTPTQDTCRCR-----PGTQPR-QDSGYKLGVD 123
      DB      141 VPCKAGHPQNTSSP--SARCPQPHTRCENQGLVEAAPGTAQSDTTCKN 185
      124 VPCPPGHF----SPGNNAQCKPWTNCTLSGKQTRHPASNSLDVAVCED 166

RESULT 10
GOHUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prote
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.

```

Genomics 13, 219-224, 1992
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to ch
A;Reference number: A38208; MUID:92250049; PMID:1315717
A;Accession: A38208
A;Molecule type: DNA
A;Residues: 1-455 <FUC>
A;Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PID:g
R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau
Cell 61, 351-359, 1990
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep
A;Reference number: A34899; MUID:90235284; PMID:2158862
A;Accession: A34899
A;Molecule type: mRNA
A;Residues: 1-455 <LOE>
A;Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A;Experimental source: placenta
A;Note: Part of this sequence, including the amino end of the mature protein, confirmed
R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.
Cell 61, 361-370, 1990
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.
A;Reference number: A34900; MUID:90235285; PMID:2158863
A;Accession: A34900
A;Molecule type: mRNA
A;Residues: 1-455 <SCH>
A;Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
R;Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaler, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A;Reference number: A36555; MUID:91090841; PMID:1702293
A;Accession: A36555
A;Molecule type: mRNA
A;Residues: 1-455 <HIM>
A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A;Accession: C36555
A;Molecule type: protein
A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;107-128;162-167,'X',169-2
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble
R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re
A;Reference number: A38281; MUID:91017509; PMID:2170974
A;Accession: A38281
A;Molecule type: mRNA
A;Residues: 1-455 <GRA>
A;Cross-references: GB:M37764
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R;Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwarg, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the typ
le form of the receptor.
A;Reference number: S12057; MUID:91006021; PMID:1698610
A;Accession: S12057
A;Molecule type: mRNA
A;Residues: 1-455 <NOP>
A;Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
R;Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A;Reference number: JT0758; MUID:94085779; PMID:8262379
A;Accession: JT0758
A;Molecule type: DNA
A;Residues: 1-13 <XEM>
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
A;Reference number: A60231; MUID:90292116; PMID:2113477
A;Accession: A60231
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Capucci, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis fact

[illegible]

A;Experimental source: kidney cell line 15
C;Genetics:
A;Gene: tnfr
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NGF>
F;211-231/Domain: transmembrane #status predicted <TMM>
F;361-447/Domain: signal transduction #status predicted <SIT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.2%; Score 206; DB 2; Length 461;
Best Local Similarity 29.4%; Pred. No. 1.8e-08;
Matches 57; Conservative 22; Mismatches 77; Indels 38; Gaps 9;
QY 18 DQEK-----EYEPQHR-ICSCRCPGTYVSAC-SRIRDVCAATCAENSYNEHMY 67
Db 36 DREKRESLCPQGYSHPQNRSTICCTGKHGTYLHNDCLGPGLDTCRECDNGTFTASENH 95
QY 68 LTTICQLCRPCDDPVMGLEIAPCTSKRTQCRQCPGMFCAAMA--LECTHCELLSDCPPG 124
Db 96 LTQCLSCSKCRSEMSQVEISPTVDRDTCGCRKNQYRKYMSETLFGCLNCSL--CPNG 152
QY 125 TE----AELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENQGLVEAPGTAQ-- 178
Db 153 TVQLPCLIEKQDTI-----CNCHSGFFLR---DKECVSVCKNADCKNLCPATSETR 201
QY 179 -----SDTCKNPL 187
Db 202 NDFQDTGTTVLLPL 215

RESULT 15
137552
OX40 homolog - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: I37552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Fonat
Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment
A;Reference number: I37552; MUID:94170844; PMID:7510240
A;Accession: I37552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 17.7%; Score 201; DB 2; Length 277;
Best Local Similarity 28.3%; Pred. No. 2.8e-08;
Matches 49; Conservative 21; Mismatches 73; Indels 30; Gaps 5;
QY 26 PQHRICSCRCPGTYVSACSRIRDVCAATCAENSYNEHMYLTICQLCRPCDPVVGLE 85
Db 37 PSNDRCHCECRPGNGVSRCSQNTVCRPCGPGFYNDVSSKP-CKPCTWCNLRSGSER 95
QY 86 IAPCTSKRTQCRQCPGMFCAAMALECTHCELLSDCPPGTEALKDEVGKGNHCVPCKA 145
Db 96 KQLCTATQDTVCRCRAG-----TQPLDSYKPGVD-----CAPCPP 130
QY 146 GHFQNTSSPSARCQPHTRCENQGLVEAPGTAQSDTTC--KNPLEPLPPMSG 196
Db 131 GHF--SPGDNQACKPWTNCTLAGKHTLQAPASNSSDAICEDRDPATQPEQTG 181

Search completed: August 28, 2004, 01:50:17
Job time : 42 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 01:33:14 ; Search time 25 Seconds

(without alignments)
410.313 Million cell updates/sec

Title: US-10-003-211-1

Perfect score: 1133

Sequence: 1 SQPQAVPPYASENQTCDQE.....QSDTCKNPLEPLPEMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	435	1 TNR3_HUMAN	P36941 homo sapien
2	771	68.0	415	1 TNR3_MOUSE	P50284 mus musculu
3	305	26.9	461	1 TR1B_HUMAN	P20333 homo sapien
4	295	26.0	474	1 TR1B_MOUSE	P25119 mus musculu
5	285.5	25.2	300	1 TR6B_HUMAN	O95407 homo sapien
6	283	25.0	625	1 TR11_MOUSE	O35305 mus musculu
7	278	24.5	277	1 TNR5_HUMAN	P25942 homo sapien
8	277	24.4	616	1 TR11_HUMAN	O9y6q6 homo sapien
9	251.5	22.2	269	1 TNR5_BOVIN	Q28203 bos taurus
10	243.5	21.5	289	1 TNR5_MOUSE	P27512 mus musculu
11	242.5	21.4	401	1 TR1B_MOUSE	O08712 mus musculu
12	239.5	21.1	401	1 TR1B_HUMAN	O00300 homo sapien
13	235.5	20.8	401	1 TR1B_MOUSE	O08727 ratu
14	230.5	20.3	283	1 TR14_HUMAN	O92956 homo sapien
15	228.5	20.2	655	1 TR21_HUMAN	O75509 homo sapien
16	226.5	20.0	655	1 TR21_MOUSE	O9epu5 mus musculu
17	225	19.9	349	1 CRMB_MOUSE	O8uyat7 camelpox vi
18	222.5	19.6	271	1 TNR4_RAT	P15725 ratu
19	214.5	18.9	272	1 TNR4_MOUSE	P47741 mus musculu
20	210.5	18.6	455	1 TR1A_HUMAN	P19438 homo sapien
21	210	18.5	349	1 CRMB_MOUSE	P34015 variola vir
22	207	18.3	351	1 CRMB_MOUSE	O73559 cowpox viru
23	206	18.2	461	1 TR1A_MOUSE	P50555 sus scrofa
24	203	17.9	323	1 TNR6_BOVIN	P51867 bos taurus
25	201	17.7	277	1 TNR4_HUMAN	P43489 homo sapien
26	201	17.7	454	1 TR1A_MOUSE	P25118 mus musculu
27	196	17.3	595	1 TNR8_HUMAN	P28908 homo sapien
28	195.5	17.3	255	1 TNR9_HUMAN	Q07011 homo sapien
29	194	17.1	332	1 TNR6_MOUSE	O77736 sus scrofa
30	189	16.7	325	1 VT2_SFVKA	P25943 Shope fibro
31	188	16.6	471	1 TR1A_BOVIN	O19131 bos taurus
32	184.5	16.3	461	1 TR1A_RAT	P22934 ratu
33	183.5	16.2	326	1 VT2_MYXVL	P29825 myxoma viru

34	182	16.1	498	1 TNR8_MOUSE	Q60846 mus musculu
35	181	16.0	335	1 TNR6_HUMAN	P25445 homo sapien
36	179.5	15.8	256	1 TNR9_MOUSE	P20333 mus musculu
37	171.5	15.1	425	1 TR16_RAT	P07174 ratu
38	167.5	14.8	440	1 TR10B_HUMAN	O14763 homo sapien
39	166	14.7	493	1 TNR8_RAT	P97525 ratu
40	164	14.5	416	1 TR16_CHICK	P18519 gallu
41	162	14.3	327	1 TNR6_MOUSE	P25446 mus musculu
42	152.5	13.5	417	1 TR16_MOUSE	O920W1 mus musculu
43	148.5	13.1	427	1 TR16_HUMAN	P08138 homo sapien
44	145.5	12.8	324	1 TNR6_RAT	Q63199 ratu
45	145	12.8	198	1 TR22_MOUSE	Q9er62 mus musculu

ALIGNMENTS

RESULT 1	
TNR3_HUMAN	
ID	TNR3_HUMAN
AC	P36941; STANDARD; PRT; 435 AA.
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Tumor necrosis factor receptor superfamily member 3 precursor
DE	(lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE	protein) (Tumor necrosis factor C receptor).
GN	LITBR OR TNFRSF3 OR TNFCR.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=93252381; PubMed=8486360;
RA	Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT	"Construction and evaluation of a hncDNA library of human 12p
RL	transcribed sequences derived from a somatic cell hybrid.";
RN	Genomics 16:214-218(1993).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length
RL	human and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[3]
RP	FUNCTIO
RX	MEDLINE=94225209; PubMed=8171323;
RA	Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA	Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT	"A lymphotoxin-beta-specific receptor.";
RL	Science 264:707-710(1994).
RN	[4]
RP	CHARACTERIZATION.

RX MEDLINE=99223511; PubMed=10207006;
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
 RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
 RT death in HeLa cells.";
 RL J. Biol. Chem. 274:11868-11873(1999).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20261554; PubMed=10799510;
 RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
 RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
 RT "The lymphotoxin-beta receptor is necessary and sufficient for
 RT LIGHT-mediated apoptosis of tumor cells.";
 RL J. Biol. Chem. 275:14307-14315(2000).
 RN [6]
 RP INTERACTION WITH TRAF3.
 RX MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RA Yagita H., Okumura K.;
 RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
 RT the lymphotoxin-beta receptor.";
 RL J. Biol. Chem. 271:14661-14664(1996).
 RN [7]
 RP INTERACTION WITH TRAF4.
 RX MEDLINE=98289299; PubMed=9626059;
 RA Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
 RA Gascogne R.D., Berern K., McFadden D., Shabaik A., Hugh J.,
 RA Reynolds A., Cleveland C.V., Reed J.C.;
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
 RT adult, fetal, and tumor tissues.";
 RL Am. J. Pathol. 152:1549-1561(1998).
 RN [8]
 RP INTERACTION WITH TRAF5.
 RX MEDLINE=98172745; PubMed=9511754;
 RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
 RA Otsuka M., Yamamoto T., Inoue J.-I.;
 RT "Cloning and characterization of a cDNA encoding the human homolog of
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
 RL Gene 207:135-140(1998).
 CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs.
 CC -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L04270; AAA36757.1; -.
 DR EMBL; BC026262; AAH26262.1; -.
 DR PIR; I54182; I54182.
 DR HSSP; P25942; 1CDF.
 DR Genew; HGNC:6718; LTBR.
 DR MIM; 600979; -.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR008063; Fas receptor.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR PRINTS; PR01680; FASRECEPTOR.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 KM Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 435
 FT DOMAIN 31 227
 FT TRANSMEM 228 248
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.

FT	DOMAIN	249	435	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	42	81	TNFR-CYS 1.
FT	REPEAT	82	124	TNFR-CYS 2.
FT	REPEAT	125	168	TNFR-CYS 3.
FT	REPEAT	169	211	TNFR-CYS 4.
FT	DISULFID	43	58	BY SIMILARITY.
FT	DISULFID	59	72	BY SIMILARITY.
FT	DISULFID	62	80	BY SIMILARITY.
FT	DISULFID	83	98	BY SIMILARITY.
FT	DISULFID	101	116	BY SIMILARITY.
FT	DISULFID	104	124	BY SIMILARITY.
FT	DISULFID	126	132	BY SIMILARITY.
FT	DISULFID	139	148	BY SIMILARITY.
FT	DISULFID	142	167	BY SIMILARITY.
FT	DISULFID	170	185	BY SIMILARITY.
FT	CARBOHYD	40	40	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	177	177	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	435 AA;	46709 MW;	624626B6022F656F CRC64;

Query Match 100.0%; Score 1133; DB 1; Length 435;
 Best Local Similarity 100.0%; Pred. No. 9.1e-90;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGYVSACSRIRDTVCATCAENS	60
Db	28	SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGYVSACSRIRDTVCATCAENS	87
QY	61	YNEHWNLTICQLCRPCDPVMGLEIADPCTSKRKTQCRCQPGMFCAMALECTHCELLSD	120
Db	88	YNEHWNLTICQLCRPCDPVMGLEIADPCTSKRKTQCRCQPGMFCAMALECTHCELLSD	147
QY	121	CPPTGEALKDEVGKNNHCVPCKAGHONTSSPSARCQPHTRCENQGLVEAAPGTAQSD	180
Db	148	CPPTGEALKDEVGKNNHCVPCKAGHONTSSPSARCQPHTRCENQGLVEAAPGTAQSD	207
QY	181	TTCKNPLEPLPEMMSGT	197
Db	208	TTCKNPLEPLPEMMSGT	224

RESULT 2
 TNFR3 MOUSE STANDARD; PRT; 415 AA.
 ID TNR3 MOUSE
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (Lymphotoxin-beta receptor).
 GN LTBR OR TNFRSF3 OR TNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX RN
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RX MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression.";
 RL J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping.";
 RL Genomics 30:312-319(1995).
 RN [3]
 RP INTERACTION WITH TRAF5.

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 37-461 FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences."; Cytokine 2:231-237(1990).
RN [7]
RP SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
RX MEDLINE=90349572; PubMed=2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor."; Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RL [8]
RN SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
RP MEDLINE=21069356; PubMed=1197692;
RX Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RA "New single nucleotide polymorphisms in the coding region of human
RT TNFR2: association with systemic lupus erythematosus."; Genes Immun. 1:501-503(2000).
RL [9]
RN SEQUENCE OF 27-31.
RP MEDLINE=90110215; PubMed=2153136;
RX Engelmann H., Novick D., Wallach D.;
RA "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors."; J. Biol. Chem. 265:1531-1536(1990).
RL [10]
RN SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RP MEDLINE=91056048; PubMed=2173696;
RX Loetscher H., Schlaepper E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).
RL [11]
RN CHARACTERIZATION.
RP MEDLINE=93016040; PubMed=1328224;
RX Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation."; J. Biol. Chem. 267:21172-21178(1992).
RL [12]
RN INTERACTION WITH TRAF2.
RP MEDLINE=94349371; PubMed=8069916;
RX Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
RA "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor."; Cell 78:681-692(1994).
RL [13]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP TRAF2.
RX MEDLINE=99221490; PubMed=10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of
RT human TRAF2."; Nature 398:533-538(1999).
RL [14]
RN VARIANTS ARG-196 AND LYS-232.
RP MEDLINE=21603988; PubMed=11762942;
RX Morita C., Horiuchi T., Tsukamoto H., Hattta N., Kikuchi Y.,
RA Arinobu Y., Otsuka T., Sawabe T., Harashima S., Nagasawa K., Niho Y.;
RT "Association of tumor necrosis factor receptor type II polymorphism

```

RT 196R with systemic lupus erythematosus in the Japanese: molecular and
RT functional analysis."
RL Arthritis Rheum. 44:2819-2827(2001).
RN [15]
RP VARIANT ARG-196.
RX MEDLINE=22151311; PubMed=12161545;
RA Peral B., San Millan J.L., Castello R., Moghetti P.,
RA Escobar-Morreale H.F.;
RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the
RT TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic
RT ovary syndrome and hyperandrogenism."
RL J. Clin. Endocrinol. Metab. 87:3977-3983(2002).
CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC approximately 5-fold lower affinity for homotrimeric
CC TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. The TNF
CC receptor 2 mediates most of the metabolic effects of TNF-alpha.
CC SUBUNIT: Binds to TRAF2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC -1- PTM: Phosphorylated; mainly on serine residues and with a very low
CC level on threonine residues.
CC -1- PTM: A soluble form (tumor necrosis factor binding protein 2) is
CC produced from the membrane form by proteolytic processing.
CC -1- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid
CC arthritis (RA). Enbrel consist of the extracellular ligand-binding
CC portion of TNFR2 linked to an Immunoglobulin Fc chain. It binds to
CC TNF-alpha and blocks its interactions with receptors.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
CC -1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC WWW="http://www.enbrel.com/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M32315; AAA59929.1; -.
DR EMBL; U52165; AAC50622.1; -.
DR EMBL; U52156; AAC50622.1; JOINED.
DR EMBL; U52157; AAC50622.1; JOINED.
DR EMBL; U52158; AAC50622.1; JOINED.
DR EMBL; U52159; AAC50622.1; JOINED.
DR EMBL; U52160; AAC50622.1; JOINED.
DR EMBL; U52161; AAC50622.1; JOINED.
DR EMBL; U52162; AAC50622.1; JOINED.
DR EMBL; U52163; AAC50622.1; JOINED.
DR EMBL; U52164; AAC50622.1; JOINED.
DR EMBL; M55994; AAA36755.1; -.
DR EMBL; AY264804; AA089076.1; -.
DR EMBL; AY342040; AAP88939.1; -.
DR EMBL; BC052977; AAH52977.1; -.
DR EMBL; S63368; AAB19824.2; -.
DR EMBL; M35857; AAA63262.1; -.
DR EMBL; AB030950; BAA89053.1; -.
DR PIR; A35356; A35356.
DR PDB; 1CA9; 12-APR-99.
DR Genew; HGNC:11917; TNFRSF1B.
Query Match 26.9%; Score 305; DB 1; Length 461;
Best Local Similarity 35.0%; Pred. No. 4.9e-19;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9
QY 5 AVPPYASE-NQTCRDQEKYYEPQHRICRCRPPGTYVSAKCSRIRDTVCATCAENSYN 63
| | | | | : | | | : | | | : | | | : | | | :
DB 28 AFTPYAPEPGSTCR--LREYYDQTAQMCSCSKSPGQHAQVFKTSTIDYCDSCEDSTYTQ 85
QY 64 HWNYLTICQLCR---PCDPVMGLEBIAPCTSKRKTQCRCQPGMFCAAWALE-CTHCELLS 119

```

```
Db      86 LMNVPECLSCGRCSSDQV-----ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLR 141
QY      120 DCPFG-----TEAEIKDEVGKGNHCVCPCAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
Db      142 KCRPFGFGVAPGTETSDV-----CKPCAPGTFSNTTSTSDICRPHQICN-----VVAIP 191
QY      175 GTAQSDTTC--KNPLEPLPP 192
Db      192 GNASMDAVCTSTSPTRSMAP 211

RESULT 4
TRIB_MOUSE
ID TRIB_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (TNF-R2) (p75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RA Kissoneghis M., Fellows R., Feldmann M., Chernajovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC approximately 5-fold lower affinity for homotrimeric
CC TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By
CC similarity).
CC -!- SUBUNIT: Binds to TRAF2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M60469; AAA39752.1; -.
DR EMBL; M59378; AAA40463.1; -.
DR EMBL; U39488; AAA85021.1; -.
RN [1]
```

```
DR EMBL; X87128; CAA60618.1; -.
DR PIR; B38634; B38634.
DR HSSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0008220; P:necrosis; IMP.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474
FT FT
FT DOMAIN 23 258 TUMOR NECROSIS FACTOR RECEPTOR
FT TRANSMEM 259 288 SUPERFAMILY MEMBER 1B.
FT DOMAIN 289 474 EXTRACELLULAR (POTENTIAL).
FT REPEAT 39 77 POTENTIAL.
FT REPEAT 78 119 CYTOPLASMIC (POTENTIAL).
FT REPEAT 120 164 TNFR-CYS 1.
FT REPEAT 165 203 TNFR-CYS 2.
FT REPEAT 203 254 TNFR-CYS 3.
FT DISULFID 40 54 TNFR-CYS 4.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 26.0%; Score 295; DB 1; Length 474;
Best Local Similarity 34.0%; Pred. No. 3.6e-18;
Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;

QY 8 PYASE-NQTRDQKEYYEPQHRICSRCPGTYVSACRSRIRDVTVCATCAENSYNHEWN 66
Db 31 PYKPEPGYEQIISQ-EYYDRKAQMCACKCPGQYVGHFCNKTSDTVCADCEASMYTQVWN 89
QY 67 YLTICQLCR--PCDPYMGIEIAPCTSKRKTKQCQPGMECA--AWALECTHCELLSDC 121
Db 90 QFRITCLSSSSCTTDQV----EIRACTKQONRVCACEAGRYCALKTHSGSCRQMRLSKC 145
QY 122 PGTEAEIKDEVGKGNHCVCPCAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDT 181
Db 146 GPGF-GVASSRAPNGNVLCACAPGTFSDTTSSDYCRPHRICS----ILAIPEGASTDA 200
QY 182 TCKNPLEPLPEMS 195
Db 201 VC----APESPTLS 210

RESULT 5
TR6B_HUMAN
ID TR6B_HUMAN STANDARD; PRT; 300 AA.
AC O95407;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).
GN TNFRSF6B OR DCR3 OR TR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```


RP SEQUENCE FROM N.A.
RC TISSUE=Fetal Lung;
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP FUNCTION: Decoy receptor for the cytotoxic ligands TNFS14/LIGHT
RC and TNFSF6/FasL. Protects against apoptosis.
RX [7]
RA [8]
RT [9]
RL [10]
RN [11]
RP [12]
RC [13]
RX [14]
RA [15]
RT [16]
RL [17]
RN [18]
RP [19]
RC [20]
RX [21]
RA [22]
RT [23]
RL [24]
RN [25]
RP [26]
RC [27]
RX [28]
RA [29]
RT [30]
RL [31]
RN [32]
RP [33]
RC [34]
RX [35]
RA [36]
RT [37]
RL [38]
RN [39]
RP [40]
RC [41]
RX [42]
RA [43]
RT [44]
RL [45]
RN [46]
RP [47]
RC [48]
RX [49]
RA [50]
RT [51]
RL [52]
RN [53]
RP [54]
RC [55]
RX [56]
RA [57]
RT [58]
RL [59]
RN [60]
RP [61]
RC [62]
RX [63]
RA [64]
RT [65]
RL [66]
RN [67]
RP [68]
RC [69]
RX [70]
RA [71]
RT [72]
RL [73]
RN [74]
RP [75]
RC [76]
RX [77]
RA [78]
RT [79]
RL [80]
RN [81]
RP [82]
RC [83]
RX [84]
RA [85]
RT [86]
RL [87]
RN [88]
RP [89]
RC [90]
RX [91]
RA [92]
RT [93]
RL [94]
RN [95]
RP [96]
RC [97]
RX [98]
RA [99]
RT [100]
RL [101]
RN [102]
RP [103]
RC [104]
RX [105]
RA [106]
RT [107]
RL [108]
RN [109]
RP [110]
RC [111]
RX [112]
RA [113]
RT [114]
RL [115]
RN [116]
RP [117]
RC [118]
RX [119]
RA [120]
RT [121]
RL [122]
RN [123]
RP [124]
RC [125]
RX [126]
RA [127]
RT [128]
RL [129]
RN [130]
RP [131]
RC [132]
RX [133]
RA [134]
RT [135]
RL [136]
RN [137]
RP [138]
RC [139]
RX [140]
RA [141]
RT [142]
RL [143]
RN [144]
RP [145]
RC [146]
RX [147]
RA [148]
RT [149]
RL [150]
RN [151]
RP [152]
RC [153]
RX [154]
RA [155]
RT [156]
RL [157]
RN [158]
RP [159]
RC [160]
RX [161]
RA [162]
RT [163]
RL [164]
RN [165]
RP [166]
RC [167]
RX [168]
RA [169]
RT [170]
RL [171]
RN [172]
RP [173]
RC [174]
RX [175]
RA [176]
RT [177]
RL [178]
RN [179]
RP [180]
RC [181]
RX [182]
RA [183]
RT [184]
RL [185]
RN [186]
RP [187]
RC [188]
RX [189]
RA [190]
RT [191]
RL [192]
RN [193]
RP [194]
RC [195]
RX [196]
RA [197]
RT [198]
RL [199]
RN [200]
RP [201]
RC [202]
RX [203]
RA [204]
RT [205]
RL [206]
RN [207]
RP [208]
RC [209]
RX [210]
RA [211]
RT [212]
RL [213]
RN [214]
RP [215]
RC [216]
RX [217]
RA [218]
RT [219]
RL [220]
RN [221]
RP [222]
RC [223]
RX [224]
RA [225]
RT [226]
RL [227]
RN [228]
RP [229]
RC [230]
RX [231]
RA [232]
RT [233]
RL [234]
RN [235]
RP [236]
RC [237]
RX [238]
RA [239]
RT [240]
RL [241]
RN [242]
RP [243]
RC [244]
RX [245]
RA [246]
RT [247]
RL [248]
RN [249]
RP [250]
RC [251]
RX [252]
RA [253]
RT [254]
RL [255]
RN [256]
RP [257]
RC [258]
RX [259]
RA [260]
RT [261]
RL [262]
RN [263]
RP [264]
RC [265]
RX [266]
RA [267]
RT [268]
RL [269]
RN [270]
RP [271]
RC [272]
RX [273]
RA [274]
RT [275]
RL [276]
RN [277]
RP [278]
RC [279]
RX [280]
RA [281]
RT [282]
RL [283]
RN [284]
RP [285]
RC [286]
RX [287]
RA [288]
RT [289]
RL [290]
RN [291]
RP [292]
RC [293]
RX [294]
RA [295]
RT [296]
RL [297]
RN [298]
RP [299]
RC [300]
RX [301]
RA [302]
RT [303]
RL [304]
RN [305]
RP [306]
RC [307]
RX [308]
RA [309]
RT [310]
RL [311]
RN [312]
RP [313]
RC [314]
RX [315]
RA [316]
RT [317]
RL [318]
RN [319]
RP [320]
RC [321]
RX [322]
RA [323]
RT [324]
RL [325]
RN [326]
RP [327]
RC [328]
RX [329]
RA [330]
RT [331]
RL [332]
RN [333]
RP [334]
RC [335]
RX [336]
RA [337]
RT [338]
RL [339]
RN [340]
RP [341]
RC [342]
RX [343]
RA [344]
RT [345]
RL [346]
RN [347]
RP [348]
RC [349]
RX [350]
RA [351]
RT [352]
RL [353]
RN [354]
RP [355]
RC [356]
RX [357]
RA [358]
RT [359]
RL [360]
RN [361]
RP [362]
RC [363]
RX [364]
RA [365]
RT [366]
RL [367]
RN [368]
RP [369]
RC [370]
RX [371]
RA [372]
RT [373]
RL [374]
RN [375]
RP [376]
RC [377]
RX [378]
RA [379]
RT

[illegible]

[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Fetal liver;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Medan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX MEDLINE=99097247; PubMed=9878548;
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANSC/OPGL; essential for
CC RANKL-mediated osteoclastogenesis. Involved in the regulation of
CC interactions between T-cells and dendritic cells.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF019046; AAB86810.1; -.
DR EMBL; BC019185; AAH19185.1; -.
DR HSSP; P25942; 1CDF.
DR MGD; MGI:1314891; Tnfrsf11a.
DR GO; GO:0007275; P:development; IMP.
DR GO; GO:0007515; P:lymph gland development; IMP.
DR GO; GO:0001503; P:ossification; IMP.
DR InterPro; IPR001368; TNFR_c6; 3.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SMO0208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 625
FT
FT DOMAIN 31 214
FT TRANSMEM 215 234
FT DOMAIN 235 625
FT REPEAT 35 69
FT REPEAT 72 113
FT REPEAT 115 152
FT REPEAT 155 195
FT DISULFID 35 47
FT DISULFID 48 61
FT DISULFID 51 69
FT DISULFID 72 87
FT DISULFID 93 113
FT DISULFID 115 128
FT CARBOHYD 106 106
FT CARBOHYD 175 175
FT CONFLICT 494 494
SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;

Query Match 25.0%; Score 283; DB 1; Length 625;
Best local Similarity 32.6%; Pred. No. 5e-17;
Matches 60; Conservative 25; Mismatches 85; Indels 14; Gaps 4;

QY 4 QAVPPASENQTCRDQEKYEYEDPHRICCSRCPPGTYSAKSGSRIRDTVCATCAENSYNE 63
Db 30 QVTPPCTQF-----RHYEHLGR-CCSRCEPGKYLSSKTPTSVCLPCGPDEYLD 79

QY 64 HNNYLTICQLCRPCDPVMGLEIAPCTSKRTQCRCQPGMFGAAMALECTHCELLSDCP 123
Db 80 TWNEEDKCLLHKVCDAKALVAVDGNHTAPRRCACTAGYH--WNSDCECCRRNTECAP 136

QY 124 GTEAEHLKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAPGTAQSDTTC 183
Db 137 GFQAQHPQLQNK-DIVCTPCLLGFPSDVFSSTDKCKPWTNCTLLGKLEAHQGTESDVVC 195

QY 184 KNPL 187
Db 196 SSSM 199

RESULT 7
TNRS_HUMAN STANDARD; PRT; 277 AA.
AC P25942; Q9BYU0;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=99356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehesvalho M.H., Laversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McIay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20.",
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM II).
RX MEDLINE=21117110; PubMed=11172023;
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.,
RT "Regulation of CD40 function by its isoforms generated through
RT alternative splicing.",
RT Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM I).
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.,
RT "Involvement of GRAF1, a relative of TRAF, in CD40 signaling.",
RL Science 267:1494-1498(1995).
RN [6]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95129692; PubMed=7530216;
RA Sato T., Irie S., Reed J.C.,
RT "A novel member of the TRAF family of putative signal transducing
RT proteins binds to the cytosolic domain of CD40.",
RL FEBS Lett. 358:113-118(1995).
RN [7]
RP INTERACTION WITH TRAF1, TRAF2, TRAF3 AND TRAF5.
RX MEDLINE=98384149; PubMed=9718306;
RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
RA Kehry M.R.,
RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)
RT interactions: regulation of CD40 signaling through multiple TRAF

RT binding sites and TRAF hetero-oligomerization.",
RL Biochemistry 37:11836-11845(1998).
RN [8]
RP INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754;
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.,
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).",
RL Gene 207:135-140(1998).
RN [9]
RP INTERACTION WITH TRAF6.
RX MEDLINE=98095703; PubMed=9432981;
RA Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,
RA Okumura K., Yamamoto T., Nagaoka H., Takemori T.,
RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates
RT extracellular signal-regulated kinase (ERK) activity in CD40
RT signaling along a ras-independent pathway.",
RL J. Exp. Med. 187:237-244(1998).
RN [10]
RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorath J., Aruffo A.,
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.",
RL Proteins 27:59-70(1997).
RN [11]
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=98266353; PubMed=9605317;
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.,
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.",
RL Protein Sci. 7:1124-1135(1998).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
RP TRAF3.
RX MEDLINE=20442386; PubMed=10984535;
RA Ni C.Z., Welsh K., Leo E., Chioi C.K., Wu H., Reed J.C., Ely K.R.,
RT "Molecular basis for CD40 signaling mediated by TRAF3.",
RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
RP TRAF3.
RX MEDLINE=22000222; PubMed=12005438;
RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
RA Satterthwait A.C., Cheng G., Ely K.R.,
RT "Downstream regulator TANK binds to the CD40 recognition site on
RT TRAF3.",
RL Structure 10:403-411(2002).
RN [14]
RP VARIANT HIGM3 ARG-83.
RX MEDLINE=21532985; PubMed=11675497;
RA Ferrari S., Gilliani S., Insalaco A., Al-Ghonatun A., Soresina A.R.,
RA Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G.,
RA Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,
RA Plebani A.,
RT "Mutations of CD40 gene cause an autosomal recessive form of
RT immunodeficiency with hyper IgM.",
RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
RN [15]
RP FUNCTION: Receptor for TNFSF5/CD40L.
CC -I- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (isoform I);
CC secreted (isoform II).
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=I;
CC IsoId=P25942-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P25942-2; Sequence=VSP_006472, VSP_006473;
CC -I- TISSUE SPECIFICITY: B-cells and in primary carcinomas.
CC -I- DISEASE: Defects in TNFRSF5 are the cause of hyper-IgM

```
CC immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an
CC autosomal recessive disorder which includes an inability of B
CC cells to undergo isotype switching, one of the final
CC differentiation steps in the humoral immune system, an inability
CC to mount an antibody-specific immune response, and a lack of
CC germinal center formation.
CC
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC DR EMBL; X60592; CAA43045.1; -.
CC DR EMBL; AL035662; CAC17670.1; -.
CC DR EMBL; AJ300189; CAC29424.1; -.
CC DR EMBL; BC012419; AAH12419.1; -.
CC DR PIR; S04460; A60771.
CC DR PDB; 1CDF; 01-APR-97.
CC DR PDB; 1FLI; 18-OCT-00.
CC DR PDB; 1LOA; 08-FEB-00.
CC DR PDB; 1CZ2; 26-SEP-01.
CC
CC Query Match 24.5%; Score 278; DB 1; Length 277;
CC Best Local Similarity 35.0%; Pred. No. 6.1e-17;
CC Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;
CC
QY 7 PPVASENQTCDQOEKEYEPQHRICSRCPGTYSAKCSRIRDTVCATCAENSYNHWN 66
Db 22 PPTA-----CR--EKQYLINSQ--CCSLQPGQKLVSDCTEFTETECLPCGESEFLDTWN 72
QY 67 YLTICQLCRPCDPVMGLEELAPCTSKRTQCRCQPGMFCAWALECTHCELLSDCPGTE 126
Db 73 RETFHGHQKYCDPNLGLRVQQKGTSETDTICTCEBGMHCTSEA--CESCVLHRS CSPFG 130
QY 127 AELKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENGIVAEAPGTASDPTTC 183
Db 131 VK-QIATGVSDTICPCPVGFNSVSSAFKCHPWTSCETKDLVVQAGTINKTDVVC 186
CC
RESULT 8
TR11_HUMAN STANDARD; PRT; 616 AA.
AC Q9Y6Q6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11A precursor
DE (Receptor activator of NF-kB) (Osteoclast differentiation factor
DE receptor) (ODFR).
GN TNFRSF11A OR RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dendritic cell;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougal W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RP FUNCTION.
RX MEDLINE=99097247; PubMed=9878548;
```

```
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
RN [3]
RP INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6.
RX MEDLINE=98447691; PubMed=9774460;
RA Wong B.R., Josien R., Lee S.Y., Vologodskaya M., Steinman R.M.,
RA Choi Y.;
RT "The TRAF family of signal transducers mediates NF-kappaB activation
RT by the TRANCE receptor.";
RL J. Biol. Chem. 273:28355-28359(1998).
RN [4]
RP VARIANT FEO LEU-LEU-CYS-ALA-LEU-LEU-21 INS, VARIANT PDB2
RP ALA-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS, AND VARIANT VAL-192.
RX MEDLINE=20082806; PubMed=10615125;
RA Hughes A.E., Ralston S.H., Marken J., Bell C., Macpherson H.,
RA Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
RA Anderson D.M.;
RT "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
RT familial expansile osteolysis.";
RL Nat. Genet. 24:45-48(2000).
CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for
CC RANKL-mediated osteoclastogenesis. Involved in the regulation of
CC interactions between T-cells and dendritic cells.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in
CC skeletal muscle, thymus, liver, colon, small intestine and adrenal
CC gland.
CC -!- DISEASE: Defects in TNFRSF11A are the cause of familial expansile
CC osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant
CC bone disorder characterized by focal areas of increased bone
CC remodelling. The osteolytic lesions develop usually in the long
CC bones during early adulthood. FEO is often associated with early
CC onset deafness and loss of dentition.
CC -!- DISEASE: Defects in TNFRSF11A are a cause of Paget disease of bone
CC 2 (PDB2) [MIM:602080]; also known as familial Paget disease of
CC bone. PDB2 is a bone remodelling disorder with clinical
CC similarities to FEO. Unlike FEO, however, affected individuals
CC have involvement of the axial skeleton with lesions in the spine,
CC pelvis and skull.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF018253; AAB86809.1; -.
CC DR HSSP; P25942; 1CDF.
CC DR Genew; HGNC:11908; TNFRSF11A.
CC DR MIM; 603499; -.
CC DR MIM; 174810; -.
CC DR MIM; 602080; -.
CC DR GO; GO:0004872; F:receptor activity; TAS.
CC DR GO; GO:0007267; P:cell-cell signaling; TAS.
CC DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
CC DR GO; GO:0007165; P:signal transduction; TAS.
CC DR InterPro; IPR001368; TNFR_c6.
CC DR Pfam; PF00020; TNFR_c6; 4.
CC DR SMART; SM00208; TNFR; 4.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 1.
CC DR PROSITE; PS50050; TNFR_NGFR_2; 1.
CC DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
CC Disease mutation; Deafness.
CC SIGNAL 1 29 POTENTIAL.
CC CHAIN 30 616 TUMOR NECROSIS FACTOR RECEPTOR
CC FT SUPERFAMILY MEMBER 11A.
```


FT	DOMAIN	30	212	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	213	233	POTENTIAL.
FT	DOMAIN	234	616	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	34	68	TNFR-CYS 1.
FT	REPEAT	71	112	TNFR-CYS 2.
FT	REPEAT	114	151	TNFR-CYS 3.
FT	REPEAT	154	194	TNFR-CYS 4.
FT	DISULFID	34	46	BY SIMILARITY.
FT	DISULFID	47	60	BY SIMILARITY.
FT	DISULFID	50	68	BY SIMILARITY.
FT	DISULFID	71	86	BY SIMILARITY.
FT	DISULFID	92	112	BY SIMILARITY.
FT	DISULFID	114	127	BY SIMILARITY.
FT	DISULFID	133	151	BY SIMILARITY.
FT	CARBOHYD	105	105	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	174	174	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	21	21	L -> LALLLCALL (in PDB2).
FT	VARIANT	21	21	/FTid=VAR 011516.
FT	VARIANT	21	21	L -> LLLCALL (in FEO).
FT	VARIANT	21	21	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTid=VAR 011518.
FT	VARIANT	192	192	/FTid=VAR 011517.
FT	VARIANT			

```

-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U57745; AAC48710.1; -.
DR      HSSP; P25942; 1CDF.
DR      InterPro; IPR008063; Fas_receptor.
DR      InterPro; IPR001368; TNFR_c6.
DR      Pfam; PF00020; TNFR_c6; 4.
DR      PRINTS; PR01680; FASRECEPTOR.
DR      SMART; SM00208; TNFR; 4.
DR      PROSITE; PS00652; TNFR_NGFR_1; 1.
DR      PROSITE; PS50050; TNFR_NGFR_2; 1.
KW      Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT      SIGNAL             1      19
FT      CHAIN              20      >269
FT                                     POTENTIAL.
FT                                     TUMOR NECROSIS FACTOR RECEPTOR
FT                                     SUPERFAMILY MEMBER 5.
FT                                     EXTRACELLULAR (POTENTIAL).
FT      DOMAIN             20      193
FT      TRANSMEM           194      215
FT      DOMAIN             216      >269
FT                                     CYTOPLASMIC (POTENTIAL).
FT      REPEAT             25      60
FT      REPEAT             61      103
FT      REPEAT             104      144
FT      REPEAT             145      187
FT      REPEAT             26      37
FT      DISULFID           38      51
FT      DISULFID           41      59
FT      DISULFID           62      77
FT      DISULFID           83      103
FT      DISULFID           105      119
FT      DISULFID           111      116
FT      DISULFID           125      143
FT      CARBOHYD           153      153
FT      CARBOHYD           180      180
FT      NON_TER            269      269
SQ      SEQUENCE           269 AA; 29983 MW; 7469033F30F95F387 CRC64;

Query Match          22.2%; Score 251.5; DB 1; Length 269;
Best Local Similarity 33.1%; Pred. No. 1.le-14;
Matches 55; Conservative 21; Mismatches 81; Indels 9; Gaps 4;

QY      20 EKEYVEPQHRICSRCPGTYVSAKSRIRDTVCATCAENSYNHEHWNLYTICQLCRPCDP 79
      ||:| | : : ||| | | : : : : : : : : | | | | | | | | | | | |
DB      28 EKQY-PVNSLCCDLCPPGQKLVNDCTEVSKTEQSCGKGFLSTWNRREKYCHEHRYCNP 85

QY      80 VMGLEEIAPCTSKRKTQCRQCPGMFCAMALECTHCELLSDCPPGTEAELEKDEVGKG--N 137
      :|| : : : | | | | | : : : : : : : : : : : : : : : : : : : : :
DB      86 NLGLRIQSEGTINTDTICVCEGQHCHTSH--CESCTPHSLCLPFGVK--QIATGLLD 140

QY      138 NHCVPCKAGHPQNTSSPSARCQPHTRCENQGLVEAPGTAQSDTTC 183
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      141 TVCEPCPLGFFSNVSSAFCKCHRWTSCEKGLVEQHVGTNKTIDVVC 186

RESULT 10
ID      TNRS_MOUSE          STANDARD;          PRT;          289 AA.
AC      P27512; Q99NE0; Q99NE1; Q99NE2; Q99NE3;
DT      01-AUG-1992 (Rel. 23, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 5 precursor
DE      (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).
GN      TNFRSF5 OR CD40.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;

```



```

RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
RL species of murine CD40 upon B lymphocyte activation.";
RN J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN=BALB/c;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM I).
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";
RL J. Immunol. 149:3921-3926(1992).
RN [4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND
RP V).
RX MEDLINE=21117110; PubMed=11172023;
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
RT "Regulation of CD40 function by its isoforms generated through
RT alternative splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
RN [5]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498(1995).
RN [6]
RP INTERACTION WITH TRAF5.
RX MEDLINE=96382484; PubMed=8790348;
RA Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,
RA Yamamoto T., Inoue J.-I.;
RT "TRAF5, a novel tumor necrosis factor receptor-associated factor
RT family protein, mediates CD40 signaling.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).
CC -!- FUNCTION: Receptor for TNFSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,
CC TRAF2 AND TRAF6 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV
CC and V); secreted (isoform II).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=I;
CC IsoId=P27512-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P27512-2; Sequence=VSP_006474, VSP_006475;
CC Name=III;
CC IsoId=P27512-3; Sequence=VSP_006477, VSP_006478;
CC Name=IV;
CC IsoId=P27512-4; Sequence=VSP_006479, VSP_006480;
CC Name=V;
CC IsoId=P27512-5; Sequence=VSP_006476;
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M83312; AAB08705.1; -.
DR EMBL; M94126; AAA37404.1; -.
DR EMBL; M94129; AAA37404.1; JOINED.
DR EMBL; M94128; AAA37404.1; JOINED.

```

DR EMBL; M94127; AAA37404.1; JOINED.
DR EMBL; AJ401387; CAC29427.1; -.
DR EMBL; AJ401388; CAC29428.1; -.
DR EMBL; AJ401389; CAC29429.1; -.
DR EMBL; AJ401390; CAC29430.1; -.
DR PIR; A46476; A46476.
DR HSSP; P25942; 1CDF.
DR MGD; MGI:88336; Tnfrsf5.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 4.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 289 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 20 193 SUPERFAMILY MEMBER 5.
FT TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 216 289 POTENTIAL.
FT REPEAT 25 60 CYTOPLASMIC (POTENTIAL).
FT REPEAT 61 103 TNFR-CYS 1.
FT REPEAT 104 144 TNFR-CYS 2.
FT REPEAT 145 187 TNFR-CYS 3.
FT DISULFID 26 37 TNFR-CYS 4.
FT DISULFID 38 51 BY SIMILARITY.
FT DISULFID 41 59 BY SIMILARITY.
FT DISULFID 62 77 BY SIMILARITY.
FT DISULFID 83 103 BY SIMILARITY.
FT DISULFID 105 119 BY SIMILARITY.
FT DISULFID 111 116 BY SIMILARITY.
FT DISULFID 125 143 BY SIMILARITY.
FT CARBOHYD 153 153 BY SIMILARITY.
FT VARSPPLIC 166 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SCEDKNLEVLQKGTSCQTNVTCGLKSRMALVIPVMG ->
FT REKVPDASPAGHSCRDGHPHHFRGVSLYQKGQETKG
FT (in isoform II).
FT /FTid=VSP 006474.
FT Missing (in isoform II).
FT /FTid=VSP 006475.
FT GLKSRMALVIPVMGILTRIFGVFLYIK -> E (in
FT isoform V).
FT /FTid=VSP 006476.
FT KKVVKPKDNMLPPARR -> SECSGEEREGGFSPEPA
FT S (in isoform III).
FT /FTid=VSP 006477.
FT Missing (in isoform III).
FT /FTid=VSP 006478.
FT KKVVKKP -> SGQETKG (in isoform IV).
FT /FTid=VSP 006479.
FT Missing (in isoform IV).
FT /FTid=VSP 006480.
FT SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;
Query Match 21.5%; Score 243.5; DB 1; Length 289;
Best Local Similarity 31.0%; Pred. No. 5.6e-14;
Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;
QY 15 TCRDQEKYYEPQHRICSRCPGTIVSAKCSRIRDVCAATCAENSYNHWNLYLTICQLC 74
Db 25 TCSD--KQYLHDGQ--CCDLQCPGSRILTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQ 80
QY 75 RPCDPVMGLLEIAPCTSKRKTQCRQCPGMFCANALECTHCELLSDCPG-----TREAEL 129
Db 81 RHCEPNOGLRVKKKEGTALASDVTCTCKEGQHCT--SKDCEACAQHTPCIPGFGVMEMATET 138
QY 130 KDEVGKGNHNCVPCAGHFONTSSPSARCQPHRCENOGIVEAAPGTAQSDTTC 183
Db 139 TDTV-----CHPCPVGFFFSNQSSLFEKCYPTWTSCEDKNLEVLQKGTSCQTNVIC 186

```

RESULT 11
T11B_MOUSE
ID T11B_MOUSE STANDARD; PRT; 401 AA.
AC 008712; 070202;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Tumor necrosis factor receptor superfamily 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
DE TNFRSF11B OR OPG OR OCIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RP STRAIN=BALB/c; TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Gander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
[2]
SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
RP AND ARG-296.
RP STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
RC MEDLINE=98382527; PubMed=9714833;
RX Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
[3]
FUNCTION.
RP MEDLINE=21060987; PubMed=10952716;
RX Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
RA Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
RA Simonet W.S.;
RT "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
RT osteoclasts and prevents vascular calcification by blocking a process
RT resembling osteoclastogenesis.";
RL J. Exp. Med. 192:463-474(2000).
-1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
its function in osteoclastogenesis. Inhibits the activation of
osteoclasts and promotes osteoclast apoptosis in vitro. Bone
homeostasis seems to depend on the local RANKL/OPG ratio. May also
play a role in preventing arterial calcification. May act as decoy
receptor for TRAIL and protect against apoptosis. TRAIL binding
blocks the inhibition of osteoclastogenesis.
-1- SUBUNIT: Homodimer.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
intestines and calvaria. Highly expressed in decidua and placenta,
and in embryo.
-1- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
whereas expression decreases at day 11 and increases from day 15
to 17. On day 15 found in developing bone primordia,
brachiocephalic artery and ductus arteriosus, left main bronchus,
abdominal aorta and midgut.
-1- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
1,25-dihydroxyvitamin D3 and parathyroid hormone.
-1- SIMILARITY: Contains 4 TNFR-Cys repeats.
-1- SIMILARITY: Contains 2 death domains.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way

```

```

modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; U94331; AAB53708.1; -.
DR EMBL; AB013898; BAA28269.1; -.
DR EMBL; AB013903; BAA33388.1; -.
DR EMBL; AB013899; BAA33388.1; JOINED.
DR EMBL; AB013900; BAA33388.1; JOINED.
DR EMBL; AB013901; BAA33388.1; JOINED.
DR EMBL; AB013902; BAA33388.1; JOINED.
DR HSSP; P25942; LCDP.
DR MGD; MGI:109587; Tnfrsf1lb.
DR GO; GO:0005578; C:extracellular matrix; IDA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT DOMAIN 198 269
FT DOMAIN 283 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT VARIANT 138 138
FT VARIANT 161 161
FT VARIANT 165 165
FT VARIANT 288 288
FT VARIANT 296 296
FT SEQUENCE 401 AA; 45923 MM; CAA6102D3B312470 CRC64;
SQ
Query Match 21.4%; Score 242.5; DB 1; Length 401;
Best Local Similarity 29.6%; Pred. No. 9.4e-14;
Matches 50; Conservative 25; Mismatches 83; Indels 11; Gaps 5;
QY YEPQ-HRICSRCPPTYVSAKSRIPTVCATCAENSYNEMNYLTICQLCRP-CDF 79
DB 30 HYDPETHQLLCRKCAFGTYLKQHCTVRKTLVPCPDHSYTDSWHTSDCIVYCSPVCKE 89
QY VMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSDCPRTGAELKDEVGKGNH 139
DB 90 LQSVKQ--ECNRTHNRVCECEEGRY----LEIEFCIKHRSCPPGS-GVVQAQTPERNTV 141
QY CVPCKAGHFQNTSSPSARCQPHTRCENOGIVEAAPGTASDTTCKNPFL 188
DB 142 CKKCPDGFSGETSSKAPCIKHTNCSTFGILLIQGNATHDNVCSGNRE 190

```

```
RESULT 12
T11B_HUMAN          STANDARD;          PRT;          401 AA.
ID   T11B_HUMAN
AC   000300; O60236; Q9UHP4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11B precursor
DE   (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN   TNFRSF11B OR OPG OR OCIF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=97262071; PubMed=9108485;
RA   Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA   Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA   Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA   Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA   Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA   Sugus S., Boyle W.J.;
RT   "Osteoprotegerin: a novel secreted protein involved in the regulation
RT   of bone density.";
RL   Cell 89:309-319(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung cancer;
RX   MEDLINE=98151033; PubMed=9492069;
RA   Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA   Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA   Tsuda E., Morinaga T., Higashio K.;
RT   "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT   osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT   osteoclastogenesis in vitro.";
RL   Endocrinology 139:1329-1337(1998).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC   TISSUE=Placenta;
RX   MEDLINE=98351569; PubMed=9688283;
RA   Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT   "Cloning and characterization of the gene encoding human
RT   osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL   Eur. J. Biochem. 254:685-691(1998).
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
```

```
RP   SEQUENCE OF 22-36 AND 378-401.
RX   MEDLINE=98238645; PubMed=9571159;
RA   Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA   Morinaga T., Tsuda E., Higashio K.;
RT   "Characterization of monomeric and homodimeric forms of
RT   osteoclastogenesis inhibitory factor.";
RL   Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN   [6]
RP   SEQUENCE OF 22-393 FROM N.A.
RC   TISSUE=Placenta;
RA   He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT   "Cloning and expression of osteoprotegerin from Homo sapiens.";
RL   Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN   [7]
RP   SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX   MEDLINE=97312536; PubMed=9168977;
RA   Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA   Morinaga T., Higashio K.;
RT   "Isolation of a novel cytokine from human fibroblasts that
RT   specifically inhibits osteoclastogenesis.";
RL   Biochem. Biophys. Res. Commun. 234:137-142(1997).
RN   [8]
RP   TRAIL BINDING.
RX   MEDLINE=98269100; PubMed=9603945;
RA   Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA   Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dadds R.A.,
RA   James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT   "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RL   J. Biol. Chem. 273:14363-14367(1998).
RN   [9]
RP   CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX   MEDLINE=98148058; PubMed=9478964;
RA   Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
RA   Morinaga T., Higashio K.;
RT   "Characterization of structural domains of human osteoclastogenesis
RT   inhibitory factor.";
RL   J. Biol. Chem. 273:5117-5123(1998).
RN   [10]
RP   REVIEW.
RX   MEDLINE=21395914; PubMed=11505389;
RA   Hofbauer L.C., Neuberger A., Heufelder A.E.;
RT   "Receptor activator of nuclear factor-kappaB ligand and
RT   osteoprotegerin: potential implications for the pathogenesis and
RT   treatment of malignant bone diseases.";
RL   Cancer 92:460-470(2001).
CC   -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC   its function in osteoclastogenesis. Inhibits the activation of
CC   osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC   homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC   play a role in preventing arterial calcification. May act as decoy
CC   receptor for TRAIL and protect against apoptosis. TRAIL binding
CC   blocks the inhibition of osteoclastogenesis.
CC   -1- SUBUNIT: Homodimer.
CC   -1- SUBCELLULAR LOCATION: Secreted.
CC   -1- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
CC   liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
CC   lymph node, trachea, adrenal gland, testis, and bone marrow.
CC   Detected at very low levels in brain, placenta and skeletal
CC   muscle. Highly expressed in fetal kidney, liver and lung.
CC   -1- INDUCTION: Upregulated by increasing calcium-concentration in the
CC   medium and estrogens. Downregulated by glucocorticoids.
CC   -1- PTM: N-glycosylated. Contains static acid residues.
CC   -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -1- SIMILARITY: Contains 2 death domains.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
```


CC	----
DR	EMBL; U94332; AAB53709.1; -. .
DR	EMBL; AB002146; BAA25910.1; -. .
DR	EMBL; AB008822; BAA32076.1; -. .
DR	EMBL; AB008821; BAA32076.1; JOINED.
DR	EMBL; BC030155; AAH30155.1; -. .
DR	EMBL; AF134187; AAF20168.1; -. .
DR	HSSP; P25942; ICDF.
DR	Genew; HGNC:11909; TNFRSF11B.
DR	MIM; 602643; -. .
DR	GO; GO:0005576; C:extracellular; TAS.
DR	GO; GO:0005125; F:cytokine activity; TAS.
DR	GO; GO:0004872; F:receptor activity; TAS.
DR	GO; GO:0007165; P:signal transduction; TAS.
DR	GO; GO:0001501; P:skeletal development; TAS.
DR	InterPro; IPR00488; Death.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 3.
DR	SMART; SM00005; DEATH; 1.
DR	SMART; SM00208; TNFR; 4.
DR	PROSITE; PS00017; DEATH_DOMAIN; FALSE_NEG.
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.
KW	Receptor; Apoptosis; Glycoprotein; Repeat; signal; Polymorphism.
FT	SIGNAL 1 21
FT	CHAIN 22 401
FT	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B.
FT	REPEAT 24 62
FT	REPEAT 65 105
FT	REPEAT 107 142
FT	REPEAT 145 185
FT	DOMAIN 198 269
FT	DOMAIN 270 365
FT	SITE 400 400
FT	DISULFID 41 54
FT	DISULFID 44 62
FT	DISULFID 65 80
FT	DISULFID 83 97
FT	DISULFID 87 105
FT	DISULFID 107 118
FT	DISULFID 124 142
FT	DISULFID 145 160
FT	DISULFID 166 185
FT	CARBOHYD 98 98
FT	CARBOHYD 152 152
FT	CARBOHYD 165 165
FT	CARBOHYD 178 178
FT	CARBOHYD 289 289
FT	VARIANT 3 3
FT	/FTId=VAR 013439.
FT	C->S: ABOLISHES DIMERIZATION.
FT	MUTAGEN 400 400
FT	MUTAGEN 400 401
FT	MUTAGEN 400 401
FT	CONFLICT 263 263
FT	D -> A (IN REF. 1).
SO	SEQUENCE 401 AA; 46040 MW; EDf448B67D86C71E CRC64;

	Query Match	21.1%;	Score 239.5;	DB 1;	Length 401;	
	Best Local Similarity	30.9%;	Pred. No. 1.7e-13;			
	Matches	Conservative 51;	Mismatches 21;	Indels 84;	Gaps 9;	
QY	25 EPQHRICCSRCPGTYVSASCSRIRDTVCAATCAENSYNHEHNNYLTIQLCRP-CDPVMG	L	L	L	L	83
Dd	34 ETSHQLLDCKCPGTYLKQHCTAKMKVCAPCPDHYYTDSMHTSDECLYCSPVKELQYV	L	L	L	L	93
QY	84 EETAPCTSRRKTQCRCQPGMFCAMALECTHCCELLSDCPRGTEAELKDEVGKNHNCVPC	L	L	L	L	143
Dd	94 KQ--ECNRTHNRVCCEKEGRY-----LEIEFCLKHRSCPPGF-GVVQAQTPEERTVCKRC	L	L	L	L	145
QY	144 KAGHFQNTSSPSARCCQPHTRCENQGLVEAAPGTAQSDTTCKNP	L	L	L	L	188
Dd	146 PDGFPSNETSSKAPCRKHNTCSVFGLLITQKGNAATHDNICSGNSE	L	L	L	L	190

RESULT 13

TT1B_RAT	TT1B_RAT	STANDARD;	PRT;	401 AA.
ID	008727;			
AC	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, last sequence update)			
DT	28-FEB-2003 (Rel. 41, last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 11B precursor (osteoprotegerin).			
DE	TNFRSF11B OR OPG.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OC	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryonic intestine;			
RX	MEDLINE=97262071; PubMed=9108485;			
RA	Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,			
RA	Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,			
RA	Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,			
RA	Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,			
RA	Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,			
RA	Suggs S., Boyle W.J.;			
RT	"Osteoprotegerin: a novel secreted protein involved in the regulation			
RT	of bone density."			
RL	Cell 89:309-319(1997).			
CC	-1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes			
CC	its function in osteoclastogenesis. Inhibits the activation of			
CC	osteoclasts and promotes osteoclast apoptosis. Bone homeostasis			
CC	seems to depend on the local RANKL/OPG ratio. May also play a role			
CC	in preventing arterial calcification. May act as decoy receptor			
CC	for TRAIL and protect against apoptosis. TRAIL binding blocks the			
CC	inhibition of osteoclastogenesis (By similarity).			
CC	-1- SUBUNIT: Homodimer (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Secreted (By similarity).			
CC	-1- INDUCTION: Upregulated by osteopontin.			
CC	-1- SIMILARITY: Contains 4 TNFR-Cys repeats.			
CC	-1- SIMILARITY: Contains 2 death domains.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U94330; AAB53707.1; -.			
DR	HSSP; P25942; 1CDF.			
DR	InterPro; IPR000488; Death.			
DR	InterPro; IPR001368; TNFR_c6.			
DR	Pfam; PF00020; TNFR_c6; 4.			
DR	SMART; SM00005; DEATH; 1.			
DR	SMART; SM00208; TNFR; 4.			
DR	PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.			
DR	PROSITE; PS00652; TNFR_NGR_1; 1.			
DR	PROSITE; PS50050; TNFR_NGR_2; 2.			
KW	Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.			
FT	SIGNAL	1	21	BY SIMILARITY.
FT	CHAIN	22	401	TUMOR NECROSIS FACTOR RECEPTOR
FT				SUPERFAMILY MEMBER 11B.
FT	REPEAT	24	62	TNFR-CYS 1.
FT	REPEAT	65	105	TNFR-CYS 2.
FT	REPEAT	107	142	TNFR-CYS 3.
FT	REPEAT	145	185	TNFR-CYS 4.
FT	DOMAIN	198	269	DEATH 1.
FT	DOMAIN	270	365	DEATH 2.
FT	SITE	400	400	INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT	DISULFID	41	54	BY SIMILARITY.
FT	DISULFID	44	62	BY SIMILARITY.
FT	DISULFID	65	80	BY SIMILARITY.
FT	DISULFID	83	97	BY SIMILARITY.
FT	DISULFID	87	105	BY SIMILARITY.

DR PDB; 1JMA; 26-SEP-01.
DR Genew; HGNC:11912; TNFRSF14.
DR MIM; 602746; -.
DR GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PRO1680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR Receptor; Transmembrane; Glycoprotein; Repeat; signal; Polymorphism;
KW 3D-structure.
FT SIGNAL 1 38
FT CHAIN 39 283
FT DOMAIN 39 202
FT TRANSMEM 203 223
FT DOMAIN 224 283
FT REPEAT 42 75
FT REPEAT 78 119
FT REPEAT 121 162
FT DISULFID 42 53
FT DISULFID 54 67
FT DISULFID 57 75
FT DISULFID 78 93
FT DISULFID 96 111
FT DISULFID 99 119
FT DISULFID 121 138
FT DISULFID 127 135
FT CARBOHYD 110 110
FT CARBOHYD 173 173
FT VARIANT 17 17
FT VARIANT 241 241
FT TURN 44 45
FT STRAND 46 46
FT STRAND 49 49
FT TURN 50 51
FT STRAND 52 52
FT STRAND 55 55
FT STRAND 57 57
FT TURN 59 60
FT STRAND 61 65
FT STRAND 74 77
FT TURN 80 81
FT STRAND 82 83
FT STRAND 88 88
FT STRAND 94 95
FT TURN 101 104
FT STRAND 105 109
FT STRAND 118 121
FT TURN 123 124
FT STRAND 125 129
FT STRAND 137 140
SQ SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;
Query Match 20.3%; Score 230.5; DB 1; Length 283;
Best Local Similarity 30.1%; Pred. No. 7.1e-13;
Matches 56; Conservative 13; Mismatches 66; Indels 51; Gaps 6;
QY 7 PPYASGNQTRDQEKYEYEPQHRICGRCPPTVYSAKCSRIRDVTCATCAENSYNHEWN 66
Db 33 PCYAPALPDSCK--EDEY--PVGSECCRCRSPGYRVKEACGELTGTVCPEPCPGTYIAHLN 88
QY 67 YLTTCQLCRPCDPVVMGLBEIAPCTSKRKTQCRQCPGMFCAWALECTHCELLSDCPGTE 126
Db 89 GLSKCLQCCQMCDDPAMGLRASRNCSTRENAVCGCSFGHFC----- 127
QY 127 AELKDEVGKGNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSDTTCKNP 186

Db 128 -----IVQGDHCAACRA---YATSSPGQRVQ-----XGTHSQDTLQCN- 164
QY 187 LEPLPP 192
Db 165 ---CPD 167
RESULT 15
TR21_HUMAN
ID TR21_HUMAN STANDARD; PRT; 655 AA.
AC 075509; Q96D86;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 21 precursor (TNFR- related death receptor-6) (Death receptor 6).
DE TNFRSF21 OR DR6.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98378343; Pubmed=9714541;
RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C., Aggarwal B.B., Ni J., Dixit V.M.;
RT "Identification and functional characterization of DR6, a novel death domain-containing TNF receptor.";
RL FEBS Lett. 431:351-356 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Parker A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Colon;
RX MEDLINE=22388257; Pubmed=12477932;
RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Uedln T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC -!- SUBUNIT: Associates with TRADD.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small intestine, colon, spleen, bone marrow and fetal liver. Very low levels were found in adult liver and peripheral blood leukocytes.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-25 is the initiator.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 01:31:38 ; Search time 115 Seconds
(without alignments)
540.496 Million cell updates/sec

Title: US-10-003-211-1
Perfect score: 1133
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTCKNPLPPLPPEMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	309.5	27.3	483	13 Q800K7	Q800K7 paralichthys
2	295.5	26.1	278	6 Q8SQ34	Q8SQ34 sus scrofa
3	291.5	25.7	433	11 Q912M6	Q912M6 rattus norv
4	291.5	25.7	474	11 Q80WY6	Q80WY6 rattus norv
5	290	25.6	459	11 Q62327	Q62327 mus musculu
6	284.5	25.1	274	6 Q7YRL5	Q7YRL5 canis famil
7	278	24.5	223	4 Q86YK5	Q86YK5 homo sapien
8	276.5	24.4	482	11 Q88734	Q88734 mus musculu
9	265.5	23.4	277	6 Q8WMQ2	Q8WMQ2 ovis aries
10	258	22.8	275	11 Q80WM9	Q80WM9 mus musculu
11	253	22.3	462	13 Q805B0	Q805B0 gallus gall
12	243.5	21.5	289	11 Q8K2X6	Q8K2X6 mus musculu
13	242.5	21.4	283	6 Q9XSZ8	Q9XSZ8 cercopithec
14	240	21.2	186	12 Q72735	Q72735 compox viru
15	238.5	21.1	318	13 Q7T2H3	Q7T2H3 oncorhynch
16	238	21.0	302	13 Q9PUS0	Q9PUS0 salvelinus

17	233.5	20.6	457	4 Q8IVS6	Q8IVS6 homo sapien
18	232.5	20.5	467	13 Q800I0	Q800I0 gallus gall
19	230	20.3	276	13 Q9DD2	Q9DD2 gallus gall
20	230	20.3	351	12 Q57117	Q57117 compox viru
21	229.5	20.3	285	13 Q90W71	Q90W71 oncorhynch
22	226.5	20.0	167	12 Q8UYL3	Q8UYL3 vaccinia vi
23	225.5	19.9	186	13 Q7ZZY5	Q7ZZY5 gallus gall
24	225.5	19.9	651	13 Q98SM6	Q98SM6 gallus gall
25	225	19.9	186	12 Q9YP87	Q9YP87 compox viru
26	225	19.9	349	12 Q57099	Q57099 monkeypox v
27	225	19.9	349	12 Q57098	Q57098 monkeypox v
28	225	19.9	349	12 Q57284	Q57284 monkeypox v
29	223	19.7	186	12 Q91LR5	Q91LR5 vaccinia vi
30	221.5	19.5	285	13 Q90YS6	Q90YS6 oncorhynch
31	221	19.5	349	12 Q57100	Q57100 monkeypox v
32	221	19.5	349	12 Q57097	Q57097 monkeypox v
33	220.5	19.5	169	11 Q9JKE0	Q9JKE0 monkeypox v
34	219	19.3	349	12 Q57102	Q57102 monkeypox v
35	219	19.3	349	12 Q57291	Q57291 monkeypox v
36	218.5	19.3	167	12 Q9DJL2	Q9DJL2 compox viru
37	218.5	19.3	350	12 Q57116	Q57116 compox viru
38	218	19.2	186	12 Q9WJB4	Q9WJB4 vaccinia vi
39	218	19.2	348	12 Q57108	Q57108 monkeypox v
40	218	19.2	348	12 Q57103	Q57103 monkeypox v
41	217.5	19.2	267	6 Q02764	Q02764 oryctolagus
42	216.5	19.1	167	12 Q72762	Q72762 compox viru
43	216	19.1	348	12 Q57277	Q57277 monkeypox v
44	216	19.1	349	12 Q57101	Q57101 monkeypox v
45	210	18.5	348	12 Q57112	Q57112 variola vir

ALIGNMENTS

RESULT 1		PRELIMINARY;		PRT;		483 AA.	
ID	Q800K7						
AC	Q800K7;						
DT	01-JUN-2003 (TREMBlrel. 24, Created)						
DT	01-JUN-2003 (TREMBlrel. 24, Last sequence update)						
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)						
DE	Tumor necrosis factor receptor-2.						
GN	TNFR-2.						
OS	Paralichthys olivaceus (Flounder).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;						
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;						
OC	Pleuronectoidae; Paralichthyidae; Paralichthys.						
OX	NCBI_TaxID=8255;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RA	Park C., Kurobe T., Hirono I., Aoki T.;						
RT	"Cloning and characterization of cDNAs for two distinct tumor necrosis						
RT	factor receptor superfamily genes from Japanese flounder Paralichthys						
RT	olivaceus."						
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; AB080947; BAC65226.1; -.						
DR	GO; GO:0004872; F:receptor activity; IEA.						
DR	InterPro; IPR001368; TNFR_c6.						
DR	Pfam; PF00020; TNFR_c6; 3.						
DR	SMART; SM00208; TNFR_4.						
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.						
DR	PROSITE; PS50050; TNFR_NGFR_2; 3.						
KW	Receptor.						
SQ	SEQUENCE 483 AA; 52227 MW; EE55874A8C7F2085 CRC64;						
Query Match 27.3%; Score 309.5; DB 13; Length 483;							
Best Local Similarity 35.4%; Pred. No. 2.9e-25;							
Matches 64; Conservative 20; Mismatches 80; Indels 17; Gaps 6;							
QY	16 CRDQEKVEYEPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNHMYLTICQLCR						75
Db	27 CHNSTTEYRQD--LCCKKCPGQRLIQKCSDATESSVCQCDSDGQYMEKWNYPQKCLISCN						84

QY 76 PCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMWALE-----CTHCELLSDCEPTGEAELEK 130
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 85 KCKSNKGLOYAQRCSSTTRTGTGCVCKPGMYC---IMDFDNPYCAECRNYSQCRAGYVSLP 141

QY 131 DEVKGN--HCVPCKAGHFONTSSPSARCQPHTRCENOGIVEAAPGTAQSDDTKNPLE 188
 || : | | | | | | | | | | : | : | : | : | : | : | : | : | : | :
Db 142 ---GKANSDVKCELCPDGMFSNTSSNTETCRPHTDCHGAIVR--KGNTTSDPVCEEGVA 196

QY 189 P 189
 |
Db 197 P 197

```

RESULT 2
08SQ34
ID Q8SQ34 PRELIMINARY; PRT; 278 AA.
AC Q8SQ34;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE CD40.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA West K.A., Li A.W., Rowden G.;
RL "Characterization of the Porcine CD40 Molecule.";
EMBL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF248545; AAL92924.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
SQ SEQUENCE 278 AA; 30951 MW; 20D446E44AF93DD2 CRC64;

```

Query Match	26.1%;	Score 295.5;	DB 6;	Length 278;
Best Local Similarity	36.9%;	Pred. No. 5.4e-24;		
Matches	62;	Conservative 19;	Mismatches 74;	Indels 13; Gaps 3,
QY	21	KEYEPEQHRICCSRCPPGTYVSAKCSRIDTVCATCAENSYNHEHWNYLTICQLCRPCDPV	80	
		: : : : : : : : : : : :		
Db	27	KENQYPTNSRCNLCPRGQKLVNHCTEVTETECLPSSSEFLATWNRKXCHQHKYCDPN	86	
QY	81	MGLEIAPCTSKRKKTQCRQCPGMFCAMALECTHCELLSDCPG-----TEAEIKDEVGK	135	
		: : : : :		
Db	87	LGLQVQREGTSKTDITTCVCSGHHCTNSA--CESCTLHSLCFPLGVKQWATEVSDTI--	142	
QY	136	GNNHCVPCKAGHPQNTSSPSARCCQPHTRCENQGLVEAPGTAQSDTTC	183	
		: : :		
Db	143	----CEPCPVGFFESNVSSASEKCCQPMTSCESKGLVEQRAGTNKTDDVVC	186	

RESULT 3		
Q91ZM6		
ID	Q91ZM6	PRELIMINARY; PRT; 433 AA.
AC	Q91ZM6;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE	Tumor necrosis factor receptor type II (Fragment).	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Osburg B., Pelser C., Doemling D., Schomburg L., Voigt K., Bickel U.
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT capillary endothelial cells and participate in TNF-alpha transport
RT through the blood-brain barrier."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF420214; AAL16021.1; "-"
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

	Query Match	25.7%;	Score 291.5;	DB 11;	Length 433;	
	Best Local Similarity	33.3%;	Pred. No. 2.3e-23;			
	Matches	65;	Conservative	24;	Mismatches 91;	Indels 15; Gaps 7;
QY	8 PYASENQTCRDQEKEYEPEOHRICTSCRCPPGTYVSAKCSRIRDTVCATCAENSYNHEHWNY	67				
Dd	11 PYKPEPBNQCQISQEXYYDKKAQMCCAKCPGGQYAKHFCKNTSDTYCADCAAGMFTQVMNH	70				
QY	68 LITICQLC-RPC--DPVGMGLEIAPCTSKRTQCRCQPBMFCA--AWALECTHCEILSDCP	122				
Dd	71 LHTCSSSSCSDDQV---ETHNCTKKONRVCACMADSYCALKLHSGNCRCQMKLSKCG	126				
QY	123 PGTEAEIKDEVGKGNNHCVPCKAGHPONTSSPSARCOQPHTRCENOGLEVAAPGTASDPTT	182				
Dd	127 PGF-GVARSRTSNGNVICSACAPGTFSPDSTTSSTDVCRPHRICS----IIAIPGNASTDAV	181				
QY	183 CKNPLEPLPEEMSGT	197				
Dd	182 CASE-SPTPSAVPRT	195				

RESULT 4		
Q80WY6		
ID	Q80WY6	PRELIMINARY; PRT; 474 AA.
AC	Q80WY6;	
DT	01-JUN-2003 (TREMBLrel. 24, Created)	
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE	Tumor necrosis factor receptor type II.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur	
OX	NCBI_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Wistar; TISSUE=Spleen;	
RA	Li Y., Ji A., Schafer M.K.;	
RT	"Expression of TNFR2 in rat dorsal root ganglion.";	
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF438039; AAP3151.1; -	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	InterPro; IPR001368; TNFR_c6.	
DR	Pfam; PF00020; TNFR_c6; 4.	
DR	SMART; SM00208; TNFR; 4.	
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.	
DR	PROSITE; PS50050; TNFR_NGFR_2; 3.	
KM	Receptor.	
SQ	SEQUENCE 474 AA; 50148 MW; 298CGAB9E8C8D714 CRC64;	

Query Match	25.7%;	Score 291.5;	DB 11;	Length 474;
Best Local Similarity	33.3%;	Pred. No. 2.6e-23;		

	Matches	65;	Conservative	24;	Mismatches	91;	Indels	15;	Gaps	7;
QY	8	PYASENQTCDQEKEYEPEQHRI	CCSRCPGTYVSAAKSRIRDTVCATCAENSYNHEMNY	67						
Dd	31	PYPKEPBGNOCCIISQEIYYDKKAQMCCAKCPGGQYAKHFENKTSDDTVCADCAAGMFTQVWNH	90							
QY	68	LTIICQLC-RPC--DPVMGLEIAPCTSKRKTQCRCQPGMFCA--AWALECTHCCELLSDCP	122							
Dd	91	LHTCLSCSSSSCSDDQV----ETHNCTKKONRVACACNAADSYCALKLHSGNCRCQCMKLSKCG	146							
QY	123	PCTEAEELKDEVEKGKNHHCVPCAAGHFONTSSPSARCOPTHRCENOGLEAAPTQAOSDTT	182							
Dd	147	PGF-GVARSRITSGNVIVCSACAAGTFSDTTSTIDCRPHRICS-----ILAIIPGNASTDAY	201							
QY	183	CKNPLEPLPPENSGT	197							
Dd	202	CASE-SPTPSAVPRT	215							

RESULT 5	ID	Q62327	PRELIMINARY;	PRT;	459 AA.
AC	Q62327;				
DT	01-NOV-1996	(TREMBLrel. 01, Created)			
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE	Murine tumour necrosis factor receptor 2 protein (Fragment) .				
GN	TNFRSF1B.				
OS	Mus musculus (Mouse) .				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=NOD;				
RA	Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;				
RT	"Amino acid variation in the tumor Necrosis factor receptor 2 is				
RL	linked to autoimmune diabetes in NOD mice.";				
RL	Genomics 0:0-0(0) .				
RP	[2]				
RP	SEQUENCE FROM N.A.				

RC	STRAIN=NOD;			
RX	MEDLINE=95178848; PubMed=7873884;			
RA	Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;			
RT	"Allelic variation of the type 2 tumor necrosis factor receptor			
RT	gene.";			
RL	Mamm. Genome 5:726-727(1994).			
RR	EMBL; X76401; CAA53981.1; -.			
DR	PIR; I48854; I48854.			
DR	HSSP; P19438; INCF.			
DR	MGD; MGI:1314883; Tnf α sf1b.			
DR	GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.			
DR	GO; GO:0006954; P:inflammatory response; IMP.			
DR	GO; GO:0008220; P:necrosis; IMP.			
DR	InterPro; IPR001368; TNFR_c6.			
DR	Pfam; PF00020; TNFR_c6; 4.			
DR	SMART; SM00208; TNFR; 4.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.			
DR	PROSITE; PS50050; TNFR_NGFR_2; 3.			
KW	Receptor.			
FT	NON TER	1	1	
FT	VARIANT	87	87	S -> T.
FT	VARIANT	93	93	T -> I.
FT	VARIANT	268	268	F -> I.
FT	VARIANT	345	345	S -> F.
FT	VARIANT	421	421	Y -> C.
SO	SEQUENCE	459 AA;	48686 MW;	6C51D2CFLC4626DF CRC64;

Query Match	25.6%;	Score 290;	DB 11;	Length 459;
Best Local Similarity	33.5%;	Pred. No. 3.6e-23;		
Matches	65;	Conservative 24;	Mismatches 85;	Indels 20;
				Gaps 8;
OY	8	PYASE-NQTCRDOEKEYEYPÖHRICCSRCPCPGTYYSAKCSRIRDTCATCAENSYNEHWN	66	

Db 16 PYKPEPEYECQISQ-EYYDRKQMCCKACPCPGQYVKHFCKNTKSDTVACADCEASMYTQVWN 74

QY 67 YLTICQLCR---PCDPVMGLEETAPCTSKRKTQCRQCPGMFCA--AMALECTHCELLSDC 121

Db 75 QFRTCLSCSSSCSTDQV----ETRACTKQQRNVCAACEAGRYCALKTHSGSCRQCMRLSKC 130

QY 122 PPGTEAELKDEVGKGNHCVPCKAGHFONTSSPSARCQPHTRCENOGLYEADPTAOSDT 181

Db 131 GPGF-GVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRICS---ILAIQNASTDA 185

QY 182 TCKNPLEPLPPEMS 195

Db 186 VC---APESPPTS 195

RESULT 6		
Q7YRL5		
ID	Q7YRL5	PRELIMINARY; PRT; 274 AA.
AC	Q7YRL5;	
DT	01-OCT-2003 (TREMBLrel. 25, Created)	
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE	CD40.	
GN	CD40.	
OS	Canis familiaris (Dog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
OX	NCBI_TaxID=9615;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Yang S., Sim G.-K.;	
RT	"Canine CD40 and CD40 Ligand cDNA Sequences.";	
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AY333789; AAP86653.1; -.	
SQ	SEQUENCE 274 AA; 30284 MW; 9723789A07FAB6DB CRC64;	

Query Match	25.1%;	Score 284.5;	DB 6;	Length 274;
Best Local Similarity	34.9%;	Pred. No. 8.4e-23;		
Matches 61;	Conservative 18;	Mismatches 89;	Indels 7;	Gaps 4

Dz
QY 9 YASENQTGRDQEKEYEYPÖHRIICCSRCPPGTYVSASKCSRIRDVTVCATCAENSYNHEWNYL 68
Db 19 XPEPRTACR--EKÖYLVD SQ--CCNMCPGEKL VNDCLHTIDTECTRCQTGEFLDTWNAE 74
QY 69 TICQLCRPCDDPVMGLEIAPCTSKRKTCRCQPGMFCAMALECETHCELLSDCPRGTEAB 12
Db 75 RHCHQHKKYCDPNLGLHVEKEGTSEITDTTCTDEGLHCTNAA--CESCTMHSLLCPPGLGVK 13
QY 129 LKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENOGIVEAAPTASTDTC 183
Db 133 -QIATGISDTCIDPCPIGFESNVSALEKCHPWTSCETKGLVKVOAGTNKTDVIC 186

RESULT 7			
Q86YK5			
ID	Q86YK5	PRELIMINARY;	PRT; 223 AA.
AC	Q86YK5;		
DT	01-JUN-2003 (TREMBLrel. 24, Created)		
DT	01-JUN-2003 (TREMBLrel. 24, last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 5 (Fragment).		
GN	TNFRSF5.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	He X., Xu L., Zeng Y.;		
RT	"Transcripts of CD40 isoform in peripheral mononuclear cells.";		
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.		
RR	EMBL; AY225405; AA043990.1; -.		

DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR	GO; GO:0005488; F:binding; IEA.
DR	GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR	GO; GO:0006915; P:apoptosis; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	GO; GO:0007165; P:signal transduction; IEA.
DR	GO; GO:0006810; P:transport; IEA.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR008063; Fas_receptor.
DR	InterPro; IPR001993; Mitoch_carrier.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 4.
DR	PRINTS; PR01680; FASRECEPTOR.
DR	SMART; SM00208; TNFR; 4.
DR	PROSITE; PS01186; EGF_2; 1.
DR	PROSITE; PS00215; MITOCH_CARRIER; 1.
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.
DR	PROSITE; PS50050; TNFR_NGFR_2; 4.
KM	Receptor.
FT	NON TER
SEQUENCE	223 AA; 24659 MW; 85G63C20BC4E0B1C CRC64;

Query Match	24.5%;	Score 278;	DB 4;	Length 223;
Best Local Similarity	35.0%;	Pred. No. 3.5e-22;		
Matches 62;	Conservative 20;	Mismatches 83;	Indels 12;	Gaps 5;

```
QY      7 PPYASENQTCDRDOEKEYEPQHRLCCSRCPPTGYVSAKCSRIRDTVCATCAENSYNEHWN    66
        |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db     22 PPTA-----CR--EKQYLINSQ---CCHIQPGKLVSDCTEFTEETECCLPCGSESHFLDTWN    72

QY      67 YLTICQLCRPCDPVMGLAEIAPCTSKRKTKQCRCQPGMFCAMALECTHCCELLSDCPPGTE    126
        |||   :|||   :|||   |||   |||   |||   |||   |||   |||   |||
Db      73 REITHQHAKYCDPNLGLRVQOKGTSETDITICTCEEGWHCTSEA--CESCVLHRSCSPFG    130

QY      127 AELKDEVKGNNHCVPCKAGHFONTSSPSARCQPHTRCENOGLEAAPGTAOSDTTC    183
        :|:   |:   |:   |:   |:   |:   |:   |:   |:   |:   |:   |:   |:
Db     131 VK-QIATGVSDTICEPQPVGFPSNVSSAFEEKHPWTSCKETKDVLVVQAGTNKTADVVC    186
```

RESULT 8

086734	PRELIMINARY;	PRT;	482 AA
ID 088734			

AC	086/54/	
DT	01-NOV-1998	(TREMBlrel. 08, Created)
DT	01-NOV-1998	(TREMBlrel. 08, Last sequence update)
DT	01-JUN-2003	(TREMBlrel. 24, Last annotation update)
DE	P80 TNF-alpha receptor.	

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN SEQUENCE FROM N.A.
 RP (1)
 RX MEDLINE=98414512; PubMed=9740674;
 RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
 RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
 and Characterization of the two Transcripts.";

RL Genomics 52:79-98 (1998)

DR	EMBL	Y14620;	CAA74969.1;	JOINED.
DR	EMBL	Y14620;	CAA74969.1;	JOINED.
DR	EMBL	Y14621;	CAA74969.1;	JOINED.
DR	EMBL	Y14622;	CAA74969.1;	JOINED.
DR	EMBL	Y14623;	CAA74969.1;	JOINED.
DR	EMBL	Y14679;	CAA74969.1;	JOINED.
DR	HSSP	Q92956;	LTMA.	

```
DR GO; GO:0004872; F:receptor activity; IEA
DR InterPro; IPR01368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
```

```
DR SMART; SM00208; TNR; 4.
DR PROSITE; PS00652; TNR_NGFR_1; 2.
DR PROSITE; PS50050; TNR_NGFR_2; 3.
```

KW Receptor. 482 AA; 51106 MW; F6C15046B48FF83C CRC64;
SQ SEQUENCE

Query Match	24.4%	Score 276.5;	DB 11;	length 482;
Best Local Similarity	32.3%;	Pred. No. 1.1e-21;		
Matches	65;	Conservative	24;	Mismatches 85;
			Indels	27;
			Gaps	9;

```

QY      8 PYASE-NQTCRDQEKEXEYEPQHRICCSRCPGTVYSAKCSRI-----RDYVCATCAEN 59
      ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :
Db     31 PYKEPGEYECQISQ-EYDRKAQMCACKCPGQYVXKHCNKTSDTVACADSDTVACADCEAS 89

```

QY 60 SYNEHWNVLTICQLCR---PCDPVMGLEETAPCTSKRKTQCRCQPGMFCA--AWALECTH 114
| : || | | | : | : | : | :
Db 90 MYTQVNQGFRTCLSSSSCSTDQV---ETPACTKQNVRVCACEAGRYCALKTHSGSCRQ 145

QY 115 CELSDCPPEGTEALIKDEVGKNNHCVPCKAGHFONTSSPSARCQPHTRCENOGIVEADP 174
146 CMRLSCGPGE - GVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRICS --- ILAIP 200

```
QY      175 GTAQSDTCKNPLEPPEMS 195
      | | : | | | : |
Db      201 GNASTDVCA---APESEPTLS 217
```

RESULT 9

Q08M02	PRELIMINARY;	PRT;	277 AA.
ID 08MM02			

AC	Q68WQ2
DT	01-MAR-2002 (TREMBlrel. 20, Created)
DT	01-MAR-2002 (TREMBlrel. 20, last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, last annotation update)

DE Membrane protein CD40 (Fragment) .

OS Ovis aries (sneep) ;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis,
OX NCBI TaxID=9940;

RP SEQUENCE FROM N.

SEQUENCE FROM N.A.

RA Zawitkowski M.S., Russ G.R., Krishnan R.;
RT "Cloning and expression of the ovine CD40 molecule and the inhibition
RT of the mixed lymphocyte reaction by the ovine CD40-EGFP fusion
RT protein.";
PI submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

protein.";
submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY072798; -;
GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR

DR GO; GO:0006915; P:apoptosis; IEA.

DR GO:0007165: P:signal transduction; IEA

DR InterPro; IPR008063; Fas_receptor-

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNER_c6; 4.

DR PRINTS; PRO1680; FASRECEP10K.
DB SWAPT: SM00208: TNEB: 4

DR SMARI; SMO0208; INER; 2;
DR PROSITE: PS00652; TNER NGER 1; 1.

DR PROSITE; PSS00050; TNFR_NGFR_2; 1.

FT	NON TER	277	277	2705308PXA182ND39	CP0644
----	---------	-----	-----	-------------------	--------

Query Match 23.4%; Score 265.5; DB 6; Length 277;

Best Local Similarity	33.7%;	Pred. No. 1e-20;							
Matches	56;	Conservative	21;	Mismatches	80;	Indels	9;	Gaps	4;

```

QY      20 EKEYEPQHRICCSRCPEGTVVSAKCSRIRDYVATCAEAENSYNEMWNYLTICQLCRPCDP 79
      ||:| | : : || |||| : | : : | | : : || ||:|
Db      28 EKQY--PVNSTCCDLCPQKLLINDCTEVSKTECQSCGKEELSTWNRREKYCHEHRYCNP 85

```

QY 80 VMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSDCPRGTEAEKDEVEKG--N 137
 : || : | | | | | : | | | | : :: |
Db 86 NLGRIQSEGLTNTDTTCVCDEGHCHTSHT--CESCTPHSLCLPFGVK---QIATGVLD 140

138 NHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAPGTAQSDTTC 183

QY

Db 141 TICEPCVGFPSNVSSAFKCHPWTSCEKGLVEQHVGTKNTDAVC 186

RESULT 10

Q80WM9 PRELIMINARY; PRT; 275 AA.

AC Q80WM9; 01-JUN-2003 (TReMBLrel. 24, Created)

DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 14 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Thymus;

RA Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;

RT "Light regulation in a murine model of ovarian carcinoma.";

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY264405; AAO89081.1; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR008063; Fas_receptor.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 4.

DR PRINTS; PRO1680; FASRECEPTOR.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS50050; TNFR_NGFR_2; 3.

KW Receptor; Signal.

FT SIGNAL 1 38 Potential.

SQ SEQUENCE 275 AA; 30171 MW; C4A7EAD8EFC0521D CRC64;

Query Match 22.8%; Score 258; DB 11; Length 275;

Best Local Similarity 34.8%; Pred. No. 6.6e-20;

Matches 63; Conservative 14; Mismatches 86; Indels 18; Gaps 6;

QY 11 SENQTCRDOEKEYEPQHRICCSRCPGTYVS AKCSRIRDTCATCAENSYNENHNYLTI 70

Db 37 SAQPSCRQEBFLVGD-----CCPMCNPGYHV KQVCSEHTGTVCAPCPPTTATHANGLSK 92

QY 71 QQLCRPCDPVMGLEIAPCTSKRKTQCRQCPGMFCAM-ALECTHCELLSDCPPTEAEL 129

Db 93 CLPCGVCDPDMGLLTWQECSSWKDITVCRCIPGYFCENQDGS HCSCTCLQHTTCPPGQRYE- 151

QY 130 KDEVGKGNH-----CVPCKAGHFQNTSSPSARCCQPHTRCENQGLVEAAPGTAQSDTTCK 184

Db 152 -----KRGTHDQDTVCADLTGTGTF-SLGGTQEBCLPWTNC-SAFQOEVRRGITNSTDTTCS 204

QY 185 N 185

Db 205 S 205

RESULT 11

Q805B0 PRELIMINARY; PRT; 462 AA.

AC Q805B0; 01-JUN-2003 (TReMBLrel. 24, Created)

DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Tumor necrosis factor receptor-II.

OS TNFR-II.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=White leghorn H-B15; TISSUE=Spleen;

RA Sayde A.A.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=White leghorn H-B15; TISSUE=Spleen;

RA Sayed A., Horuchi H., Furusawa S., Matsuda H.;

RT "Molecular cloning and characterization of chicken Tumor necrosis factor receptor-II (TNFR-II) and Tumor necrosis factor receptor associated factor-5 (TRAF-5) genes.";

RT Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; AB101004; BAC55966.1; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR008063; Fas_receptor.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 3.

DR PRINTS; PRO1680; FASRECEPTOR.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00652; TNFR_NGFR_1; 2.

DR PROSITE; PS50050; TNFR_NGFR_2; 3.

KW Receptor.

SQ SEQUENCE 462 AA; 50141 MW; 8B00A93305414782 CRC64;

Query Match 22.3%; Score 253; DB 13; Length 462;

Best Local Similarity 29.4%; Pred. No. 3.9e-19;

Matches 59; Conservative 24; Mismatches 100; Indels 18; Gaps 6;

QY 8 PYASENQTCRDOEKEYEPQHRICCSRCPGTYVS AKCSRIRDTCATCAENSYNENHNY 67

Db 23 PYTPQSAQCRNPSTEFYERLKKCCSKCPPGQKAESCSHSVDTKCIPCLPDTTAVWNR 82

QY 68 LITCQLCR-PCDPVMGLEIAPCTSKRKTQCRQCPGMFCAMALE-CTHCELLSDCPPGT 125

Db 83 SPQCFACSPPCR-KGYENQTCITLSWDRICSCPNEYCISKMYONCHICKVHKKCGRGY 140

QY 126 EAEIKDEVKGNHNCVPCKAGHFQNTSSPSARCCQPHTRCENQGLVEAAPGTAQSDTTCKN 185

Db 141 RVSRRG-TDSTDTECKPCPPGTFSDESYDTSCTPHTVCKS----VAVAGNNVNDTVCHD 195

QY 186 PLEP-----LPPEMSGT 197

Db 196 SVATALLPHTAVNFLPSQSSST 216

RESULT 12

Q8K2X6 PRELIMINARY; PRT; 289 AA.

AC Q8K2X6; 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Similar to tumor necrosis factor receptor superfamily, member 5.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC029254; AAH29254.1; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0005840; C:ribosome; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PRO1680; FASRECEPTOR.
DR SMART; SMO0208; TNFR_4.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
XN Receptor.
SQ SEQUENCE 289 AA; 32077 MW; DBE93B1E439F1E2A CRC64;

	Query Match	21.5%;	Score 243.5;	DB 11;	Length 289;	
	Best Local Similarity	31.0%;	Pred. No. 2.6e-18;			
	Matches	54;	Conservative	22;	Mismatches	81;
					Indels	17;
					Gaps	5,
QY	15 TCEDQEKEYEPQHRI	CSCRCPGTYVS	AKCSRIRDTVCATCAENS	YHEHNYLTICQLC	74	
Dd	25 TCSDD--KQYLHDGQ--CCDL	CGPSRLTSHCTALBKTC	CHPCDGSSESAQNREIR	CHQH	80	
QY	75 RCPDPVWGLEIETAPCTSKRK	TQCRCQPMFCAMALECTHCE	LSDCPDG----	TEAEL	129	
Dd	81 RHCFPNQGLRVKKEGTAESD	TVCACKEQQHCT--SKDC	EACAGHTPCLPGFVMEM	ATET	138	
QY	130 KDEYFGKNNHCVPCKAGH	FONTSSBSARCQPHTRCENOG	LVEAAPGTASD	TTTC	183	
Dd	139 TDFTV-----CHPCPV	GFESSNOSSLFEKCYPWTS	CEDKNLEVLQKGTSQT	NVIC	186	

```

RESULT 13
Q9XSZ8
ID Q9XSZ8 PRELIMINARY; PRT; 283 AA.
AC Q9XSZ8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hveas.
GN HVEAS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99296730; PubMed=10366573;
RA Foster T.P., Chouljenko V.N., Kousoulas K.G.;
RT "Functional characterization of the HveA homolog specified by African
RT green monkey kidney cells with a herpes simplex virus expressing the
RT green fluorescence protein.";
RL Virology 258:365-374(1999).
DR EMBL; AF147720; AAD37381.1; -.
DR HSSP; Q92956; 1JMA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.

```

SEQ	SEQUENCE	283 AA;	30199 MW;	397951C6617FE3AA	CRC64;				
QY	Query Match	21.4%;	Score 242.5;	DB 6;	Length 283;				
	Best Local Similarity	32.2%;	Pred. No. 3.3e-18;						
	Matches	57;	Conservative 18;	Mismatches 85;	Indels 17; Gaps 6				
QY	9	YASENOTCRDQEKYEYEPQRI	CCSRCPGT	YVSAKCS	RIRDTVCATCAENS	YNEHWN	YL 68		
		::	::	::	::	::			
DB	35	YAPALPSCK--EDEY--	PVSGECCPKCGP	GFHVRA	CGEQTGT	VECPSC	PGTYIAHF	NGL 90	
QY	69	TICQLCRPCDPVMGLE	ELIAPCTSK	RKTQCR	QCPGM	FCAM--	ALECTHCELL	SDCPGTEA 127	
		::	::	::	::	::	::		
DB	91	SKCLQCQCMCDPAMGL	RTSRNCST	TYANAL	CGCSP	GFHCCI	IQDDH	CAACRAYATSSP	g--- 147
QY	128	ELKDEVGKGNH-----	CVPCKAGH	FQNTSS	PSAR	CQPHTR	CENQGL	VEAAPGTAQS 179	
		::	::	::	::	::	::	::	
DB	148	---QRVQKG	GESQDTLCQNC	CPGTG	--SSNG	TLBECQ	HGNKCS	KWLVT	EAGPGTSSS 200

RESULT	14
ID	072735
PRT;	186 AA.
PRELIMINARY;	
AC	072735;
DT	01-AUG-1998 (TREMBlrel. 07, Created)
DT	01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	A56R protein.
GN	A56R.
OS	Cowpox virus (CPV).
OC	viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae
CC	Orthopoxvirus.
OX	NCBI_TaxID=10243;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=GRI-90;
RC	MEDLINE=98229462; PubMed=9568042;
RA	Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA	Ryazankina O.I., Gutarov V.V., Kotwal G.J.;
RT	"Species-specific differences in genome organization of cowpox,
RT	smallpox, and vaccinia viruses.";
RL	Virology 243:432-460(1998) .
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=GRI-90;
RC	MEDLINE=97068532; PubMed=89632248;
RA	Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,
RA	Shchelkunov S.N., Sandakhchiev L.S.;
RT	"Genes of a circle of hosts for the cowpox virus.";
RL	Dokl. Akad. Nauk 349:829-833(1996) .
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=GRI-90;
RA	Shchelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V.,
RA	Ryazankina O.I., Petrov N.A., Gutarov V.V., Kotwal G.J.,
RA	Sandakhchiev L.S.;
RT	"Structure-function and organization of cowpox virus strain GRI-90
RT	complete genome.";
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A.
RC	STRAIN=GRI-90;
RA	Totmenin A.V.;
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; X94355; CAD90723.1; -.
DR	HSSP; Q92956; IMA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPR001368; TNER C6.
DR	Pfam; PF00020; TNER_C6; 2.
DR	SMART; SM00208; TNER_2.
DR	PROSITE; PS00652; TNER_NGFR_1; 2.
DR	PROSITE; PS50050; TNER_NGFR_2; 2.
DR	SEQUENCE 186 AA; 20482 MW; D2342F1040A00AE3 CRC64;

iris Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 01:44:58 ; Search time 32 Seconds
(without alignments)
317.822 Million cell updates/sec

Title: US-10-003-211-1
Perfect score: 1133
Sequence: 1 SQQAVPPYASENOTCRDQE.....QSDTCKNPLEPLPEMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1133	100.0	197	2	US-08-505-606-1	Sequence 1, Appli
2	1133	100.0	197	4	US-09-000-166-1	Sequence 1, Appli
3	1133	100.0	197	4	US-09-303-262-1	Sequence 1, Appli
4	987	87.1	170	4	US-08-828-683A-14	Sequence 14, Appli
5	981	86.6	170	4	US-09-523-323-57	Sequence 57, Appli
6	771	68.0	415	3	US-09-006-353A-6	Sequence 6, Appli
7	771	68.0	415	4	US-09-573-986-6	Sequence 3, Appli
8	456	40.2	77	3	US-08-866-545-3	Sequence 48, Appli
9	456	40.2	77	4	US-09-627-775-3	Sequence 3, Appli
10	305	26.9	227	3	US-08-974-022-48	Sequence 48, Appli
11	305	26.9	227	3	US-08-795-445A-48	Sequence 48, Appli
12	305	26.9	227	3	US-08-795-447A-48	Sequence 48, Appli
13	305	26.9	227	3	US-08-974-186-48	Sequence 48, Appli
14	305	26.9	227	3	US-08-795-446B-48	Sequence 48, Appli
15	305	26.9	227	3	US-08-795-446B-48	Sequence 48, Appli
16	305	26.9	227	4	US-08-706-945D-134	Sequence 134, App
17	305	26.9	227	4	US-08-577-788C-48	Sequence 48, Appli
18	305	26.9	235	4	US-09-326-394-4	Sequence 2, Appli
19	305	26.9	235	4	US-09-580-235-2	Sequence 2, Appli
20	305	26.9	235	4	US-09-580-235-8	Sequence 2, Appli
21	305	26.9	235	4	US-09-580-181-2	Sequence 2, Appli
22	305	26.9	235	4	US-09-580-181-8	Sequence 2, Appli
23	305	26.9	235	4	US-09-102-530-2	Sequence 2, Appli
24	305	26.9	235	4	US-09-102-530-8	Sequence 2, Appli
25	305	26.9	257	4	US-09-579-845-10	Sequence 10, Appli
26	305	26.9	461	1	US-08-385-229-2	Sequence 2, Appli
27	305	26.9	461	2	US-08-650-000-2	Sequence 2, Appli
			461	3	US-09-042-785A-7	Sequence 7, Appli

28	305	26.9	461	3	US-08-477-347-3	Sequence 3, Appli
29	305	26.9	461	3	US-09-006-353A-4	Sequence 4, Appli
30	305	26.9	461	3	US-08-476-862-2	Sequence 2, Appli
31	305	26.9	461	4	US-09-573-986-4	Sequence 4, Appli
32	305	26.9	461	4	US-08-406-824A-2	Sequence 2, Appli
33	305	26.9	461	4	US-09-800-909-2	Sequence 2, Appli
34	305	26.9	461	4	US-09-758-124-2	Sequence 2, Appli
35	305	26.9	461	4	US-09-800-908-3	Sequence 3, Appli
36	305	26.9	461	6	5395760-2	Patent No. 5395760
37	305	26.9	486	1	US-08-243-010-1	Sequence 1, Appli
38	305	26.9	518	1	US-08-385-229-4	Sequence 4, Appli
39	305	26.9	518	4	US-09-579-845-1	Sequence 1, Appli
40	305	26.9	518	4	US-09-579-845-3	Sequence 3, Appli
41	304	26.8	235	4	US-09-580-235-4	Sequence 4, Appli
42	304	26.8	235	4	US-09-580-235-6	Sequence 6, Appli
43	304	26.8	235	4	US-09-580-181-4	Sequence 4, Appli
44	304	26.8	235	4	US-09-580-181-6	Sequence 6, Appli
45	304	26.8	235	4	US-09-102-530-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-505-606-1
Sequence 1, Application US/08505606
Patent No. 5925351

GENERAL INFORMATION:

APPLICANT: BROWNING, Jeffrey L.
APPLICANT: BENJAMIN, Christopher D.
APPLICANT: HOCHMAN, Paula S.
TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND
TITLE OF INVENTION: ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS
TITLE OF INVENTION: THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr.
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,606
FILING DATE: 21-JUL-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/378,968
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-505-606-1

Query Match 100.0%; Score 1133; DB 2; Length 197;


```
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-828-683A-14

Query Match      87.1%; Score 987; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENSYNEHWNYYLTICQLC 74
      |||||||
DB      1 TCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENSYNEHWNYYLTICQLC 60

QY      75 RPCDPVMGLEIEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSDCPPGTEAELKDEVG 134
      |||||||
DB      61 RPCDPVMGLEIEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSDCPPGTEAELKDEVG 120

QY      135 KGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGLVEAAPGTAQSDTTCK 184
      |||||||
DB      121 KGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGLVEAAPGTAQSDTTCK 170

RESULT 5
US-09-523-323-57
; Sequence 57, Application US/09523323
; Patent No. 6635743
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000C
; CURRENT APPLICATION NUMBER: US/09/523,323
; EARLIER FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/168,380
; EARLIER FILING DATE: 1999-12-02
; EARLIER APPLICATION NUMBER: 60/148,326
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/142,657
; EARLIER FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 60/137,457
; EARLIER FILING DATE: 1999-06-04
```

```
; EARLIER APPLICATION NUMBER: 60/124,041
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 09/252,656
; EARLIER FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: 60/075,409
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/027,287
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: 60/013,923
; EARLIER FILING DATE: 1996-03-22
; EARLIER APPLICATION NUMBER: 60/030,157
; EARLIER FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (7)
; OTHER INFORMATION: May be any amino acid
US-09-523-323-57
```

```
Query Match      86.6%; Score 981; DB 4; Length 170;
Best Local Similarity 99.4%; Pred. No. 4.3e-85;
Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      15 TCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENSYNEHWNYYLTICQLC 74
      |||||||
DB      1 TCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENSYNEHWNYYLTICQLC 60

QY      75 RPCDPVMGLEIEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSDCPPGTEAELKDEVG 134
      |||||||
DB      61 RPCDPVMGLEIEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSDCPPGTEAELKDEVG 120

QY      135 KGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGLVEAAPGTAQSDTTCK 184
      |||||||
DB      121 KGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGLVEAAPGTAQSDTTCK 170
```

```
RESULT 6
US-09-006-353A-6
; Sequence 6, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```

; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-006-353A-6

```

Query Match	68.0%;	Score 771;	DB 3;	Length 415;
Best Local Similarity	70.7%;	Pred. No. 7.1e-65;		
Matches 135; Conservative	14;	Mismatches 40;	Indels 2;	Gaps 1;

```
QY      1 SQQAAPPYASENOTCRDQEKEYEPEOHRICCSRCPGTYVSAKCSRIDTVCATCAENS   60
        ||||| ||||| :||||| :||||| :||| :||| |||
Db     28 SQQLPVPYRIENOTCWDQDKEEYEPMHDVCCSRCPGEFVFVAVCSRSQDTVCKTCPHNS   87
QY      61 YNEHWNYYLTICQLCRPCDPVMGLBEIAPCTSKRKTQCRCQPGMFCAAWALECTHC--ELL  118
        |||||:::||||| |:||:||||| :||||| | ||||| |||
Db     88 YNEHWNHLSTCQLCRPCDIVLGFEEVAPCTSDRKAEKRCQPGMSCVYLNDNECVACHEERL  147
QY     119 SDCPPTGAELKDVEVGKNNHCVPCPKAGHFONTSSPARCOPHTRCENOGIYEAPGTAQ  178
        | |||||::||| ::||| | ||||| ||||| ||||| ||||| :
Db    148 VLCQPGTEAEVTDEIMDTDVNCVPCPKBGHONTSSPARCQPHTRCEIOGLVEAABGTSY  207
QY     179 SDTTCKNPLEP  189
        ||| ||||| |||
Db    208 SDTICKNPPEP  218
```

```

RESULT 7
US-09-573-986-6
; Sequence 6, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573, 986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-6

```

Query Match	68.0%;	Score 771;	DB 4;	length 415;
Best Local Similarity	70.7%;	Pred. No. 7.1e-65;		
Matches 135;	Conservative 14;	Mismatches 40;	Indels 2;	Gaps 1;
QY	1	SQPQAVDPYASENQTCRDQKEKEYEHPQHRICCSRCPGTYVSACSRIRDTVCATCAENS	60	
		: : :		
Db	28	SQPOLVDPYRIENQTCWMDQKEYEHPMHDDVCCSRCPGEFVFAYCSRSQDPTVCCKTCPHNS	87	
QY	61	YNEHNMVLLTICQLCRPCDPVMGLEETIAPCTSKRKTQCRQCPGMFCAMALECTHC--ELL	118	
		: : : :		
Db	88	YNEHNMHLLSTCQLCRPCDILVGFEEVAPCTSDRKAECCRCQPGMSCVYLLDNECVHCEEERL	147	
QY	119	SDCPPTGEAELEKDEVGKGNNHCVCPCKAGHFQNTSSPSARCPQPHTRCENQGLVEAAPGTAQ	178	
		: : : :		
Db	148	VLCQPGTEAEVLTDEIMDTDVNVCVCPCKGHHFQNTSSPRARCPQPHTRCEIQGLVEAAPGTSY	207	

QY	179	SDTTCKNPLEP	189
Db	208	SDTICKNPPPEP	218

RESULT 8
 US-08-866-545-3
 ; Sequence 3, Application US/08866545
 ; Patent No. 6265535
 ; GENERAL INFORMATION:
 ; APPLICANT: Greene, Mark I.
 ; APPLICANT: Murali, Ramachandran
 ; APPLICANT: Takasaki, Wataru
 ; TITLE OF INVENTION: PEPTIDES AND PEPTIDE
 ; TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
 ; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
 ; TITLE OF INVENTION: USES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ;

ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,545
FILING DATE: 30-MAY-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009113-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265535e
US-08-866-545-3

Query Match	40.2%	Score 456;	DB 3;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 5.1e-36;		
Matches 77;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

RESULT 9
US-09-627-775-3
; Sequence 3, Application US/09627775
; Patent No. 6682739
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark

APPLICANT: Murali, Ramachandran
APPLICANT: Aoki, Kazuhiro
APPLICANT: Baron, Roland
TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
FILE REFERENCE: UPN3832
CURRENT APPLICATION NUMBER: US/09/627,775
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146,090
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-627-775-3

Query Match 40.2%; Score 456; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 5.1e-36;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSNEHWNLTICQLCRPCDPMGLBEIAPCTSKRTQCRCQPGMFCAMALE 111
Db 1 VCATCAENSNEHWNLTICQLCRPCDPMGLBEIAPCTSKRTQCRCQPGMFCAMALE 60
QY 112 CTHCELLSDCPRPGTEAE 128
Db 61 CTHCELLSDCPRPGTEAE 77

RESULT 10
US-08-974-022-48
Sequence 48, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-48
Query Match 26.9%; Score 305; DB 3; Length 227;

Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
QY 5 AVPPYASE-NQTCRDQKEYEPQHRICCSRCPPTGVSAKCSRIKDTVCATCAENSYN 63
Db 28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSIDTVCDSCEDSTYTQ 85
QY 64 HMNLTICQLCR--PCDPVMGLBEIAPCTSKRTQCRCQPGMFCAMALE-CTHCELLS 119
Db 86 LMNWVPECLSCGSRSSDQV---ETQACTREQNRICTCRPGWCALSKQEGCRLCAPLR 141
QY 120 DCPPG-----TEALKDEYVGKNNHCVPCKAGHFQNTSSPSARQCPHTRCENQGLVEAP 174
Db 142 KCRPGFGVARPGTETSDV-----CKPCARGTFSNTTSSDTICRPHQICN----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLRP 192
Db 192 GNASRDVACTSTSPTRSMAP 211

RESULT 11
US-08-795-445A-48
Sequence 48, Application US/08795445A
Patent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
QY 5 AVPPYASE-NQTCRDQKEYEPQHRICCSRCPPTGVSAKCSRIKDTVCATCAENSYN 63
Db 28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKVFCTKTSIDTVCDSCEDSTYTQ 85
QY 64 HMNLTICQLCR--PCDPVMGLBEIAPCTSKRTQCRCQPGMFCAMALE-CTHCELLS 119
Db 86 LMNWVPECLSCGSRSSDQV---ETQACTREQNRICTCRPGWCALSKQEGCRLCAPLR 141

QY 120 DCPG-----TEAEIKDEVGKNNHCVPCKAGHPONTSSPSARCQPHTRCENQGLVEAP 174
Db 142 KCRPGFGVARPGTETS DVV-----CKPCAPGTFSTNTSSDTCRPHQICN-----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 192 GNASRDVAVCTSTSPTRSMAP 211

RESULT 12

US-08-795-447A-48
; Sequence 48, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-447A-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
QY 5 AVPPYASE-NQTRDQEKYEYEPQHRICSRCPGTYVSACKSRIRDTCATCAENS YNE 63
Db 28 AFTPYAPEPGSTCR--LREYYDQTAQWCCSKCSPGQHAKVCTKTS DTVCDSCEDSTYTQ 85
QY 64 HNNYLITICQLCR---PCDPVWGLEIEIAPCTSKRKTQCRQPGMFCAMALE-CTHCELLS 119
Db 86 LNNWVPECLSCGSRSSDQV---ETQACTREQNRICTCRPGWYCALSKQEGCRICAPLR 141
QY 120 DCPG-----TEAEIKDEVGKNNHCVPCKAGHPONTSSPSARCQPHTRCENQGLVEAP 174
Db 142 KCRPGFGVARPGTETS DVV-----CKPCAPGTFSTNTSSDTCRPHQICN-----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 192 GNASRDVAVCTSTSPTRSMAP 211

RESULT 13
US-08-974-186-48
; Sequence 48, Application US/08974186

; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-186-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
QY 5 AVPPYASE-NQTRDQEKYEYEPQHRICSRCPGTYVSACKSRIRDTCATCAENS YNE 63
Db 28 AFTPYAPEPGSTCR--LREYYDQTAQWCCSKCSPGQHAKVCTKTS DTVCDSCEDSTYTQ 85
QY 64 HNNYLITICQLCR---PCDPVWGLEIEIAPCTSKRKTQCRQPGMFCAMALE-CTHCELLS 119
Db 86 LNNWVPECLSCGSRSSDQV---ETQACTREQNRICTCRPGWYCALSKQEGCRICAPLR 141
QY 120 DCPG-----TEAEIKDEVGKNNHCVPCKAGHPONTSSPSARCQPHTRCENQGLVEAP 174
Db 142 KCRPGFGVARPGTETS DVV-----CKPCAPGTFSTNTSSDTCRPHQICN-----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 192 GNASRDVAVCTSTSPTRSMAP 211

RESULT 14
US-08-795-446B-48
; Sequence 48, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
;

STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-446B-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTCRDQEKYYEPQHRICCSRCPGTYVSAAKSRIRDVTCATCAENSYNE 63
Db 28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKEVCTKTSDTVCDSCEDSTYTQ 85
QY 64 HWNVLTICQLCR--PCDPVMGLEELAPCTSKRKTQCRQCPGMFCAMALE-CTHCELLS 119
Db 86 LMNWVPECLSCGSRSSDQV---ETQACTREQNRICTCRPGWCALSKQEGCRLCAPLR 141
QY 120 DCPPG-----TEAEIKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
Db 142 KCRPGFGVAPGTETSDV-----CKPCAPGTFSNTTSTIDICRPHQICN----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 192 GNASRDVAVCTSTSPTRSMAP 211

RESULT 15
US-08-706-945D-134
Sequence 134, Application US/08706945D
Patent No. 6369027
GENERAL INFORMATION:
APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
PRIOR APPLICATION NUMBER: 1996-09-03
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentn version 3.1
SEQ ID NO 134
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-08-706-945D-134

Query Match 26.9%; Score 305; DB 4; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
QY 5 AVPPYASE-NQTCRDQEKYYEPQHRICCSRCPGTYVSAAKSRIRDVTCATCAENSYNE 63
Db 28 AFTPYAPEPGSTCR--LREYYDQTAQMCCSKCSPGQHAKEVCTKTSDTVCDSCEDSTYTQ 85
QY 64 HWNVLTICQLCR--PCDPVMGLEELAPCTSKRKTQCRQCPGMFCAMALE-CTHCELLS 119
Db 86 LMNWVPECLSCGSRSSDQV---ETQACTREQNRICTCRPGWCALSKQEGCRLCAPLR 141
QY 120 DCPPG-----TEAEIKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAP 174
Db 142 KCRPGFGVAPGTETSDV-----CKPCAPGTFSNTTSTIDICRPHQICN----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 192 GNASRDVAVCTSTSPTRSMAP 211

Search completed: August 28, 2004, 01:50:54
Job time : 33 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 01:47:13 ; Search time 125 Seconds
(without alignments)
495.830 Million cell updates/sec

Title: US-10-003-211-1
Perfect score: 1133
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPEMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	197	13	US-10-003-211-1 Sequence 1, Appli
2	1133	100.0	435	9	US-09-907-372-19 Sequence 19, Appl
3	1133	100.0	435	9	US-09-768-779A-6 Sequence 6, Appli
4	1133	100.0	435	10	US-09-917-372-19 Sequence 19, Appl
5	1133	100.0	435	12	US-10-087-192-942 Sequence 942, App
6	1133	100.0	435	14	US-10-291-480-6 Sequence 6, Appli
7	1133	100.0	435	15	US-10-369-300-17 Sequence 17, Appl
8	1133	100.0	435	15	US-10-262-445-133 Sequence 133, App
9	1129	99.6	399	9	US-09-907-372-1 Sequence 1, Appli
10	1129	99.6	399	10	US-09-917-372-1 Sequence 1, Appli
11	987	87.1	170	13	US-10-112-793-14 Sequence 14, Appl
12	970	85.6	172	15	US-10-375-680-57 Sequence 57, Appl
13	780	68.8	257	9	US-09-948-018-19 Sequence 19, Appl
14	771	68.0	402	12	US-10-087-192-939 Sequence 939, App
15	771	68.0	415	9	US-09-826-212-6 Sequence 6, Appli

16	771	68.0	415	9	US-09-907-372-20	Sequence 20, Appl
17	771	68.0	415	9	US-09-935-727-8	Sequence 8, Appli
18	771	68.0	415	10	US-09-917-372-20	Sequence 20, Appl
19	771	68.0	415	14	US-10-186-643-6	Sequence 6, Appli
20	771	68.0	415	15	US-10-418-242-8	Sequence 8, Appli
21	381.5	33.7	305	15	US-10-264-049-3058	Sequence 3058, Ap
22	311.5	27.5	659	14	US-10-363-427-12	Sequence 12, Appl
23	307	27.1	720	14	US-10-363-427-8	Sequence 8, Appli
24	305	26.9	225	9	US-09-840-795-10	Sequence 10, Appl
25	305	26.9	227	11	US-09-405-032-131	Sequence 131, App
26	305	26.9	235	9	US-09-907-263-4	Sequence 4, Appli
27	305	26.9	235	10	US-09-882-735-16	Sequence 16, Appl
28	305	26.9	235	12	US-10-621-783-4	Sequence 4, Appli
29	305	26.9	235	12	US-10-622-383-4	Sequence 2, Appli
30	305	26.9	235	14	US-10-243-230-2	Sequence 8, Appli
31	305	26.9	235	14	US-10-243-230-8	Sequence 75, Appl
32	305	26.9	235	14	US-10-436-826-75	Sequence 10, Appl
33	305	26.9	257	14	US-10-313-852-10	Sequence 10, Appl
34	305	26.9	257	14	US-10-314-033-10	Sequence 226, App
35	305	26.9	439	15	US-10-360-101-226	Sequence 3, Appli
36	305	26.9	450	9	US-09-768-779A-3	Sequence 2, Appli
37	305	26.9	450	14	US-10-291-480-3	Sequence 3, Appli
38	305	26.9	461	9	US-09-800-909-2	Sequence 2, Appli
39	305	26.9	461	9	US-09-826-212-4	Sequence 4, Appli
40	305	26.9	461	9	US-09-758-124-2	Sequence 2, Appli
41	305	26.9	461	9	US-09-896-096A-17	Sequence 17, Appl
42	305	26.9	461	9	US-09-894-924-17	Sequence 17, Appl
43	305	26.9	461	9	US-09-840-707A-17	Sequence 17, Appl
44	305	26.9	461	9	US-09-800-908-3	Sequence 3, Appli
45	305	26.9	461	9	US-09-935-727-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-003-211-1
; Sequence 1, Application US/10003211
; Publication No. US20020197254A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Soluble Lymphotoxin Beta Receptor and
; TITLE OF INVENTION: Anti-Lymphotoxin Receptor and Ligand Antibodies as
; TITLE OF INVENTION: Therapeutic Agents for the Treatment of Immunological
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: A013US
; CURRENT APPLICATION NUMBER: US/10/003,211
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: PCT/US97/19436
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/029,060
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-003-211-1

Query Match 100.0%; Score 1133; DB 13; Length 197;
Best Local Similarity 100.0%; Pred. No. 7.6e-89;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SQPQAVPPYASENQTCRDQEKEYEPQHRICSRCPGTYVSAKCSRIRDYVCAICAENS	60
DB	1	SQPQAVPPYASENQTCRDQEKEYEPQHRICSRCPGTYVSAKCSRIRDYVCAICAENS	60
QY	61	YNEHMWNYLTICQLCRPCDPVGMGLEIAPCTSKRTQCRCQPGMFCAMWALECTHCELLSD	120
DB	61	YNEHMWNYLTICQLCRPCDPVGMGLEIAPCTSKRTQCRCQPGMFCAMWALECTHCELLSD	120

```
QY      121  CPBGTEAEIKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENOGGLVEAAPGTAQSD 180
      |||||||
Db      121  CPBGTEAEIKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENOGGLVEAAPGTAQSD 180

QY      181  TTCKNPLEPLPEMSGT 197
      |||||||
Db      181  TTCKNPLEPLPEMSGT 197

RESULT 2
US-09-907-372-19
; Sequence 19, Application US/09907372
; Patent No. US20020068242A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/907,372
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020068242A1 g339762
US-09-907-372-19
```

```
Query Match      100.0%; Score 1133; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSACKSRIRDTVCATCAENS 60
      |||||||
Db      28  SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSACKSRIRDTVCATCAENS 87

QY      61  YNEHWNLYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMWALECTHCELLSD 120
      |||||||
Db      88  YNEHWNLYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMWALECTHCELLSD 147

QY      121  CPBGTEAEIKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENOGGLVEAAPGTAQSD 180
      |||||||
Db      148  CPBGTEAEIKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENOGGLVEAAPGTAQSD 207

QY      181  TTCKNPLEPLPEMSGT 197
      |||||||
Db      208  TTCKNPLEPLPEMSGT 224
```

```
RESULT 3
US-09-768-779A-6
; Sequence 6, Application US/09768779A
; Patent No. US20020127637A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: MOORE, PAUL
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
; RECEPTOR-LIKE PROTEIN 8
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/768,779A
; FILING DATE: 25-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/086,582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KENLEY K. HOOVER
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF368PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-768-779A-6
```

```
Query Match      100.0%; Score 1133; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSACKSRIRDTVCATCAENS 60
      |||||||
Db      28  SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSACKSRIRDTVCATCAENS 87

QY      61  YNEHWNLYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMWALECTHCELLSD 120
      |||||||
Db      88  YNEHWNLYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMWALECTHCELLSD 147

QY      121  CPBGTEAEIKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENOGGLVEAAPGTAQSD 180
      |||||||
Db      148  CPBGTEAEIKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENOGGLVEAAPGTAQSD 207

QY      181  TTCKNPLEPLPEMSGT 197
      |||||||
Db      208  TTCKNPLEPLPEMSGT 224
```

```
RESULT 4
US-09-917-372-19
; Sequence 19, Application US/09917372
; Publication No. US20030068619A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/917,372
; CURRENT FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030068619A1 g339762
US-09-917-372-19
```

```
Query Match      100.0%; Score 1133; DB 10; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSACKSRIRDTVCATCAENS 60
```

```
Db      28 SGPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTCATCAENS 87
QY      61 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRTQCRCPGMFCAAWALECTHCELLSD 120
Db      88 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRTQCRCPGMFCAAWALECTHCELLSD 147
QY      121 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 180
Db      148 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 207
QY      181 TTCKNPLEPLPEMSGT 197
Db      208 TTCKNPLEPLPEMSGT 224
```

```
RESULT 5
US-10-087-192-942
; Sequence 942, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 942
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-942
```

```
Query Match      100.0%; Score 1133; DB 12; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTCATCAENS 60
Db      28 SGPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTCATCAENS 87
QY      61 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRTQCRCPGMFCAAWALECTHCELLSD 120
Db      88 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRTQCRCPGMFCAAWALECTHCELLSD 147
QY      121 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 180
Db      148 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 207
QY      181 TTCKNPLEPLPEMSGT 197
Db      208 TTCKNPLEPLPEMSGT 224
```

```
RESULT 6
US-10-291-480-6
; Sequence 6, Application US/10291480
; Publication No. US20030100069A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
; FILE REFERENCE: PF368C1D1
; CURRENT APPLICATION NUMBER: US/10/291,480
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/768,779
```

```
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/086,582
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/048,020
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 435
; TYPE: PRT
; ORGANISM: human
US-10-291-480-6
```

```
Query Match      100.0%; Score 1133; DB 14; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SGPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTCATCAENS 60
Db      28 SGPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTCATCAENS 87
QY      61 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRTQCRCPGMFCAAWALECTHCELLSD 120
Db      88 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRTQCRCPGMFCAAWALECTHCELLSD 147
QY      121 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 180
Db      148 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 207
QY      181 TTCKNPLEPLPEMSGT 197
Db      208 TTCKNPLEPLPEMSGT 224
```

```
RESULT 7
US-10-369-300-17
; Sequence 17, Application US/10369300
; Publication No. US20030215442A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher
; APPLICANT: Hancock, Wayne
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
; TITLE OF INVENTION: IMMUNE
; TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY
; FILE REFERENCE: 7853-255
; CURRENT APPLICATION NUMBER: US/10/369,300
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/358,463
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-300-17
```

```
Query Match      100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SGPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTCATCAENS 60
Db      28 SGPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTCATCAENS 87
QY      61 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRTQCRCPGMFCAAWALECTHCELLSD 120
Db      88 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRTQCRCPGMFCAAWALECTHCELLSD 147
QY      121 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 180
Db      148 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 207
```

QY 181 TTCKNPLELPPEMSGT 197
Db 208 TTCKNPLELPPEMSGT 224

RESULT 8
US-10-262-445-133

; Sequence 133, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Zhong, Hainong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
; FILE REFERENCE: 21402-462D
; CURRENT APPLICATION NUMBER: US/10/262,445
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 133
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-445-133

Query Match 100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGGTYVSAAKCSRIRDTVCATCAENS 60
Db 28 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGGTYVSAAKCSRIRDTVCATCAENS 87

QY 61 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 120
Db 88 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 180
Db 148 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 207
QY 181 TTCKNPLELPPEMSGT 197
Db 208 TTCKNPLELPPEMSGT 224

RESULT 9

US-09-907-372-1
; Sequence 1, Application US/09907372
; Patent No. US20020068242A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/907,372
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020068242A1 7497867CD1
US-09-907-372-1

Query Match 99.6%; Score 1129; DB 9; Length 399;
Best Local Similarity 99.5%; Pred. No. 3.5e-88;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGGTYVSAAKCSRIRDTVCATCAENS 60
Db 28 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGGTYVSAAKCSRIRDTVCATCAENS 87
QY 61 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 120
Db 88 YNEHWNVLTICQLCRPCDPVMGLEIAPCTSKRKTQCRCQPGMFCAMALECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 180
Db 148 CPPGTEAELKDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAQSD 207
QY 181 TTCKNPLELPPEMSGT 197
Db 208 TTCKNPLELPPEMSGT 224

RESULT 10

US-09-917-372-1
; Sequence 1, Application US/09917372
; Publication No. US20030068619A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/917,372
; CURRENT FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030068619A1 7497867CD1
US-09-917-372-1

Query Match 99.6%; Score 1129; DB 10; length 399;
Best Local Similarity 99.5%; Pred. No. 3.5e-88;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENS 60
Db 28 SOPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENS 87
QY 61 YNEHWNLYTICQLCRPCDPVPMGLBEIAPCTSKRKTQCRCQPGMFCAMWALBECTHCELLSD 120
Db 88 YNEHWNLYTICQLCRPCDPVPMGLBEIAPCTSKRKTQCRCQPGMFCAMWALBECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
Db 148 CPPGTEAELKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCCKNPLEPLPEMSGT 197
Db 208 TTCCKNPLEPLPEMSGS 224

RESULT 11
US-10-112-793-14
; Sequence 14, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: Amino Acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-112-793-14

Query Match 87.1%; Score 987; DB 13; Length 170;

Best Local Similarity 100.0%; Pred. No. 1.9e-76;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TCRDQEKYEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENSYNHWNLYTICQLC 74
Db 1 TCRDQEKYEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENSYNHWNLYTICQLC 60
QY 75 RPPCDPVMGLBEIAPCTSKRKTQCRCQPGMFCAMWALBECTHCELLSDCPPGTEAELKDEVG 134
Db 61 RPPCDPVMGLBEIAPCTSKRKTQCRCQPGMFCAMWALBECTHCELLSDCPPGTEAELKDEVG 120
QY 135 KGNHCVPCCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 184
Db 121 KGNHCVPCCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 170

RESULT 12
US-10-375-680-57
; Sequence 57, Application US/10375680
; Publication No. US20040009147A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000E
; CURRENT APPLICATION NUMBER: US/10/375,680
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,234
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-375-680-57

Query Match 85.6%; Score 970; DB 15; length 172;
Best Local Similarity 98.3%; Pred. No. 5.3e-75;
Matches 169; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 15 TCRDQE--KEYEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENSYNHWNLYTICQ 72
Db 1 TCRDQEXAAEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENSYNHWNLYTICQ 60
QY 73 LCRPCDPVMGLBEIAPCTSKRKTQCRCQPGMFCAMWALBECTHCELLSDCPPGTEAELKDE 132
Db 61 LCRPCDPVMGLBEIAPCTSKRKTQCRCQPGMFCAMWALBECTHCELLSDCPPGTEAELKDE 120
QY 133 VGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 184
Db 121 VGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 172

RESULT 13
US-09-948-018-19
; Sequence 19, Application US/09948018
; Patent No. US20020150977A1
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37677
; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05

```
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-948-018-19
```

```
Query Match          68.8%; Score 780; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      63 EHMWNYLTICQLCRPCDPVVMGLEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCP 122
      |||
Db       1 EHMWNYLTICQLCRPCDPVVMGLEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCP 60

QY      123 PGTEAEIKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTT 182
      |||
Db       61 PGTEAEIKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTT 120

QY      183 CKNPLEPLPEMSGT 197
      |||
Db       121 CKNPLEPLPEMSGT 135
```

```
RESULT 14
US-10-087-192-939
; Sequence 939, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 939
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-939
```

```
Query Match          68.0%; Score 771; DB 12; Length 402;
Best Local Similarity 70.7%; Pred. No. 1.2e-57;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;
```

```
QY      1 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTYSASAKSRIRDTVCATCAENS 60
      |||
Db       41 SQPQLVPPYRIENQTCWDQDKEYEYEPMDVCCSRCPGEEFVFAVCSRSQDTVCKTCPHNS 100

QY      61 YNEHWNLYTICQLCRPCDPVVMGLEIAPCTSKRKTQCRCQPGMFCAAWALECTHC--ELL 118
      |||
Db       101 YNEHWNHLSCTQLCRPCDVLGFEEVAPCTSDRAKBCRCQPGMSCVYILDNECVHCEEERL 160

QY      119 SDCPPGTEAEIKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQ 178
      |||
Db       161 VLCQPGTEAEVTDIMDTDVCNCPCKPGHFQNTSSPRARCQPHTRCEIQGLVEAAPGTSTY 220

QY      179 SDTCKNPLEP 189
      |||
Db       221 SDTCKNPPEP 231
```

```
RESULT 15
US-09-826-212-6
; Sequence 6, Application US/09826212
```

```
; Patent No. US20010021516A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280006
; CURRENT APPLICATION NUMBER: US/09/826,212
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-212-6
```

```
Query Match          68.0%; Score 771; DB 9; Length 415;
Best Local Similarity 70.7%; Pred. No. 1.2e-57;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;
```

```
QY      1 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTYSASAKSRIRDTVCATCAENS 60
      |||
Db       28 SQPQLVPPYRIENQTCWDQDKEYEYEPMDVCCSRCPGEEFVFAVCSRSQDTVCKTCPHNS 87

QY      61 YNEHWNLYTICQLCRPCDPVVMGLEIAPCTSKRKTQCRCQPGMFCAAWALECTHC--ELL 118
      |||
Db       88 YNEHWNHLSCTQLCRPCDVLGFEEVAPCTSDRAKBCRCQPGMSCVYILDNECVHCEEERL 147

QY      119 SDCPPGTEAEIKDEVGKGNHCVPCCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQ 178
      |||
Db       148 VLCQPGTEAEVTDIMDTDVCNCPCKPGHFQNTSSPRARCQPHTRCEIQGLVEAAPGTSTY 207

QY      179 SDTCKNPLEP 189
      |||
Db       208 SDTCKNPPEP 218
```

Search completed: August 28, 2004, 01:53:06
Job time : 128 secs